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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 11.5 Seconds

(without alignments)
278.878 Million cell updates/sec

Title: US-09-620-586b-12

Perfect score: 630
Sequence: 1 DFGLDDEHSTSRRCRYPL.....EGQIYKIPAMVVDRCGS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	630	100.0	375	US-08-891-789B-2
2	630	100.0	375	US-09-252-149B-2
3	630	100.0	375	US-09-252-149B-31
4	618	98.1	126	US-08-525-596B-6
5	618	98.1	126	US-09-177-860A-6
6	618	98.1	126	US-09-378-238-6
7	618	98.1	126	US-09-451-501-6
8	618	98.1	130	US-09-378-238-21
9	618	98.1	225	US-09-378-238-19
10	618	98.1	375	US-08-525-596B-14
11	618	98.1	375	US-08-765-875-5
12	618	98.1	375	US-08-795-671-5
13	618	98.1	375	US-09-177-860A-14
14	618	98.1	375	US-09-252-149B-29
15	618	98.1	375	US-09-252-149B-32
16	618	98.1	375	US-09-252-149B-34
17	618	98.1	375	US-09-252-149B-35
18	618	98.1	375	US-09-378-238-14
19	618	98.1	375	US-09-451-501-14
20	618	98.1	375	US-09-451-501-19
21	618	98.1	375	US-09-451-501-21
22	618	98.1	375	US-09-451-501-23
23	618	98.1	375	US-09-451-501-25
24	618	98.1	376	US-08-525-596B-12
25	618	98.1	376	US-09-177-860A-12
26	618	98.1	376	US-08-891-789B-6
27	618	98.1	376	US-09-252-149B-27

28	618	98.1	376	US-09-252-149B-28	Sequence 28, Appl
29	618	98.1	376	US-09-378-238-12	Sequence 12, Appl
30	618	98.1	376	US-09-451-501-12	Sequence 12, Appl
31	618	98.1	376	US-09-451-501-25	Sequence 25, Appl
32	612	97.1	375	US-09-252-149B-30	Sequence 25, Appl
33	608	96.5	375	US-09-252-149B-33	Sequence 33, Appl
34	579	91.9	108	US-08-525-596B-8	Sequence 8, Appl
35	579	91.9	108	US-09-378-238-8	Sequence 8, Appl
36	579	91.9	108	US-09-451-501-8	Sequence 8, Appl
37	579	91.9	108	US-09-177-860A-8	Sequence 8, Appl
38	573.5	91.0	124	US-09-252-149B-24	Sequence 24, Appl
39	573	91.0	126	US-08-247-907A-2	Sequence 24, Appl
40	573	91.0	126	US-08-452-772-2	Sequence 2, Appl
41	573	91.0	126	US-08-765-875-4	Sequence 2, Appl
42	573	91.0	126	US-08-795-671-4	Sequence 4, Appl
43	573	91.0	126	US-09-414-234-2	Sequence 2, Appl
44	573	91.0	126	US-08-919-850-2	Sequence 2, Appl
45	573	91.0	126	PCT-US94-05288-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-891-789B-2
Sequence 2, Application US/08891789B
Patent No. 6103466
GENERAL INFORMATION:
APPLICANT: Grobet, Luc; Georges, Michel
TITLE OF INVENTION: Double-Muscling in Mammals
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
STATE: Ontario
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,789B
FILING DATE: July 14, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 52836/00004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-891-789B-2

Query Match 100.0%; Score 630; DB 3; Length 375;
Best local similarity 100.0%; Pred. No. 5.9e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTSRRCRYPLTVDFEAFGDMWITAPRYKANYSGSGCEVFLOKYPHTL 60
DB 267 DFGLDDEHSTSRRCRYPLTVDFEAFGDMWITAPRYKANYSGSGCEVFLOKYPHTL 326
QY 61 VHOANRSGAGCCPTPTMSPINMLYNGSGQIYYGKIPAMVVDRCGS 109
DB 327 VHOANRSGAGCCPTPTMSPINMLYNGSGQIYYGKIPAMVVDRCGS 375

RESULT 2

US-09-252-149B-2
 / Sequence 2, Application US/09252149B
 / Patent No. 6369201
 / GENERAL INFORMATION:
 / APPLICANT: Barker, Christopher A.
 / APPLICANT: Morsey, Mohamed
 / TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
 / VERTEBRATE SUBJECTS
 / FILE REFERENCE: 9001-0042
 / CURRENT APPLICATION NUMBER: US/09/252,149B
 / PRIOR FILING DATE: 1999-02-18
 / PRIOR APPLICATION NUMBER: 60/075,213
 / NUMBER OF SEQ ID NOS: 39
 / SOFTWARE: Patent In Ver. 2.0
 / SEQ ID NO 2
 / LENGTH: 375
 / TYPE: PRT
 / ORGANISM: bos taurus
 US-09-252-149B-2

Query Match 100.0%; Score 630; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.9e-66;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 60
 DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 3

US-09-252-149B-31
 / Sequence 31, Application US/09252149B
 / Patent No. 6369201
 / GENERAL INFORMATION:
 / APPLICANT: Barker, Christopher A.
 / APPLICANT: Morsey, Mohamed
 / TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
 / VERTEBRATE SUBJECTS
 / FILE REFERENCE: 9001-0042
 / CURRENT APPLICATION NUMBER: US/09/252,149B
 / PRIOR FILING DATE: 1999-02-18
 / PRIOR APPLICATION NUMBER: 60/075,213
 / NUMBER OF SEQ ID NOS: 39
 / SOFTWARE: Patent In Ver. 2.0
 / SEQ ID NO 31
 / LENGTH: 375
 / TYPE: PRT
 / ORGANISM: bos taurus
 US-09-252-149B-31

Query Match 100.0%; Score 630; DB 4; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.9e-66;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 60
 DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 4

US-08-525-596B-6

/ Sequence 6, Application US/08525596B
 / Patent No. 5827733
 / GENERAL INFORMATION:
 / APPLICANT: Huynh, Thanh
 / APPLICANT: Lee, Se-Jin
 / TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
 / NUMBER OF SEQUENCES: 32
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fish & Richardson P.C.
 / STREET: 4225 Executive Square, Suite 1400
 / CITY: La Jolla
 / STATE: CA
 / COUNTRY: US
 / ZIP: 92037
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / OPERATING SYSTEM: Windows95
 / SOFTWARE: FastSeq for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/525,596B
 / FILING DATE: 19-SEP-1995
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US94/07762
 / FILING DATE: 08-JUL-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Wechterell, Jr., Ph.D, John R.
 / REGISTRATION NUMBER: 31,678
 / REFERENCE/DOCKET NUMBER: 07265/075001
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 619-678-5099
 / TELEFAX: 619-678-5070
 / INFORMATION FOR SEQ ID NO: 6:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 126 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / FRAGMENT TYPE: internal
 US-08-525-596B-6

Query Match 98.1%; Score 618; DB 2; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4.2e-65;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 60
 DB 18 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEPFLQKYPHTL 77
 QY 61 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 78 VHOANPRGSAGPCCPTTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 126

RESULT 5

US-09-177-860A-6
 / Sequence 6, Application US/09177860A
 / Patent No. 6096506
 / GENERAL INFORMATION:
 / APPLICANT: Huynh, Thanh
 / APPLICANT: Lee, Se-Jin
 / TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Gray Cary Ware & Freidenrich LLP
 / STREET: 4365 Executive Drive, Suite 1600
 / CITY: San Diego
 / STATE: CA
 / COUNTRY: US
 / ZIP: 92121
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D. Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-6

Query Match 98.1%; Score 618; DB 3; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 60
DB 18 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 126

RESULT 6
US-09-378-238-6
Sequence 6, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEOTIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JH01120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 126
TYPE: PRT
ORGANISM: Mus musculus
US-09-378-238-6

Query Match 98.1%; Score 618; DB 4; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 60

DB 18 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 126

RESULT 7
US-09-451-501-6
Sequence 6, Application US/09451501
Patent No. 6468535
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESS: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,071
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US94/03019
FILING DATE: 18-March-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-451-501-6

Query Match 98.1%; Score 618; DB 4; Length 126;
Best Local Similarity 98.2%; Pred. No. 4.2e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 60
DB 18 DFGLDDEHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYGCEGCEVFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 126

RESULT 8
US-09-378-238-21
Sequence 21, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin

APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
FILE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 130
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-378-238-21

Query Match 98.1%; Score 618; DB 4; Length 130;
Best Local Similarity 98.2%; Pred. No. 4.3e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
DB 22 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 81
QY 61 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 82 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 130

RESULT 9
US-09-378-238-19
Sequence 19, Application US/09378238
Patent No. 6465239
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
FILE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JHU1120-9
CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 225
TYPE: PRT
ORGANISM: Gallus gallus
US-09-378-238-19

Query Match 98.1%; Score 618; DB 4; Length 225;
Best Local Similarity 98.2%; Pred. No. 8.3e-65;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 177 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 225

RESULT 10
US-08-525-596B-14
Sequence 14, Application US/08525596B
Patent No. 5827733
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-525-596B-14

Query Match 98.1%; Score 618; DB 2; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
DB 267 DFLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPKMSPIINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 11
US-08-765-875-5
Sequence 5, Application US/08765875
Patent No. 5914234
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLAY HORN JUBAS & LUBITZ

```
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-765-875-5

Query Match      98.1%; Score 618; DB 2; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGDCCDHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGEGEFVFLQKYPTHTL 60
DB 267 DFGDCCDHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGEGEFVFLQKYPTHTL 326

OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 12
US-08-795-671-5
Sequence 5, Application US/08795671
Patent No. 6008434
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
```

```
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GDF-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-795-671-5

Query Match      98.1%; Score 618; DB 3; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGDCCDHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGEGEFVFLQKYPTHTL 60
DB 267 DFGDCCDHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGEGEFVFLQKYPTHTL 326

OY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 13
US-09-177-860A-14
Sequence 14, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
```

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; FRAGMENT TYPE: Internal
US-09-177-860A-14

Query Match 98.1%; Score 618; DB 3; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 14
US-09-252-149B-29
; Sequence 29, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-149B-29

Query Match 98.1%; Score 618; DB 4; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

RESULT 15
US-09-252-149B-32
; Sequence 32, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-252-149B-32

Query Match 98.1%; Score 618; DB 4; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.5e-64;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGIDCDHSTESRCRYPITVDPEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

Search completed: January 31, 2003, 18:18:23
Job time : 11.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 32 Seconds
(without alignments)
453.885 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630
Sequence: 1 DFGJDCDEHSTSRRCRYPL.....EGQIYKIPAMVVDRCGS 109

Scoring table: BLOSUM62

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
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23:	/SID2/gcgatc/geneseq/geneseqp_emb1/A12002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	630	100.0	109	22	AAB20142	Cattle growth diff
2	630	100.0	375	19	AAW69887	Bovine growth diff
3	630	100.0	375	20	AAV33934	Amino acid sequenc
4	630	100.0	375	20	AAV31917	Bovine myostatin s
5	630	100.0	375	20	AAV31917	Bovine GDF-8 prot
6	630	100.0	375	22	AAB20135	Cattle growth diff
7	630	100.0	375	23	AAE18664	Bovine myostatin
8	630	100.0	375	23	AAE18664	Bovine myostatin
9	634	95.0	375	20	AAW97884	Bovine myostatin
10	618	98.1	109	22	AAB20141	Human growth diffe

1	618	98.1	109	23	AAAM51935
2	618	98.1	126	15	AAAR63161
3	618	98.1	126	19	AAAM69883
4	618	98.1	126	20	AAAY15386
5	618	98.1	126	22	AAAR73182
6	618	98.1	130	22	AAAR73189
7	618	98.1	160	22	AAAB20153
8	618	98.1	226	22	AAAR73188
9	618	98.1	254	22	AAAB20152
10	618	98.1	362	22	AAAB20132
11	618	98.1	374	23	AAAU75623
12	618	98.1	375	15	AAAR63160
13	618	98.1	375	19	AAAM69888
14	618	98.1	375	19	AAAM69891
15	618	98.1	375	19	AAAM69885
16	618	98.1	375	19	AAAM65460
17	618	98.1	375	19	AAAM65460
18	618	98.1	375	20	AAAY13839
19	618	98.1	375	20	AAAY13980
20	618	98.1	375	20	AAI33841
21	618	98.1	375	20	AAAY13843
22	618	98.1	375	20	AAAY13844
23	618	98.1	375	20	AAAY33937
24	618	98.1	375	20	AAAY33938
25	618	98.1	375	20	AAAY33932
26	618	98.1	375	20	AAAY33935
27	618	98.1	375	20	AAAY33935
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29	618	98.1	375	20	AAAY33935
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35	618	98.1	375	20	AAAY33935
36	618	98.1	375	20	AAAY33935
37	618	98.1	375	20	AAAY33935
38	618	98.1	375	20	AAAY33935
39	618	98.1	375	20	AAAY33935
40	618	98.1	375	20	AAAY33935
41	618	98.1	375	21	AAAB21087
42	618	98.1	375	21	AAAB21087
43	618	98.1	375	21	AAAY75566
44	618	98.1	375	22	AAAB73187
45	618	98.1	375	22	AAAB20131

ALIGNMENTS

RESULT 1
AAB20142

DT 30-APR-2001 (first entry)

DE Cattle growth differentiation factor 8 C-terminal region.

KM Growth differentiation factor 8; GDF-8; myostatin; down-regulation
KM vaccine; muscle; meat; cachexia; cardiant; cattle; mutant; mutein.

OS Bos taurus.
OS Synthetic.

PN W0200105820-A2.

PD 25-JAN-2001

PF 20-JUL-2000; 2000WO-DK00413.

PR 20-JUL-1999; 99DK-0001014.
PR 26-JUL-1999; 99US-0145275.
XX

PA (MEBI-) M & E BIOTECH AS.
XY

Pl Halkier T, Mouritsen S, Klysner S,
XX

PT Increasing the muscle mass of animals used in meat production by down regulating growth differentiation factor 8 (GDF-8) activity in the

PT animal through induction of anti-GDF-8 antibody production -

XX Claim 17; Page 94-95; 110pp; English.

CC The present sequence comprises the 109 amino acid residue
CC C-terminal region of cattle growth differentiation factor 8
CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
CC AAB20132). The homodimer of this region is thought to be the
CC biologically active form of GDF-8. It is an object of the
CC invention to produce a recombinant therapeutic vaccine capable of
CC effecting down-regulation of GDF-8 in order to increase the muscle
CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-55)
CC are provided that are capable of breaking autoinhibition against
CC autologous GDF-8. These comprise the C-terminal portion of human
CC GDF-8 in which a portion of the native sequence is replaced by a
CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
CC P2 or P30. The high number of Cys residues in the C-terminal region
CC limits the possible sites in which the T-cell epitope can be
CC positioned without major disturbance of the native 3-dimensional
CC structure of the protein. Nucleic acids encoding the GDF-8 variants
CC can be used for genetic immunisation of the animals. Down-regulation
CC of GDF-8 activity can increase muscle mass by up to at least 45% in
CC cattle, pigs and poultry used for meat production, reducing the need
CC for antibiotic feed-additives. Anti-GDF-8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.

XX Sequence 109 AA;

Query Match 100.0%; Score 630; DB 22; Length 109;
Best local similarity 100.0%; Pred. No. 1, 8e-59;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTSRCCRYPLTVDFEAFGMDWIAPKRYKANYSGCEPEFLQKYPHTL 60
DB 1 DFGLDDEHSTSRCCRYPLTVDFEAFGMDWIAPKRYKANYSGCEPEFLQKYPHTL 60

OY 61 VHQNPRGSGAGPCCPTPKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 61 VHQNPRGSGAGPCCPTPKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109

RESULT 2

AAW69887 standard; Protein; 375 AA.

XX AAW69887;

XX 07-DEC-1998 (first entry)

XX Bovine growth differentiation factor-8.

XX Growth differentiation factor-8; GDF-8; human; transgenic animal;

XX transforming growth factor-beta; muscle; meat; inhibitor; obesity;

XX neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;

XX therapy.

XX Bos taurus.

XX Key

XX Cleavage-site

XX Protein

XX Label= Mat_protein

XX MO9833887-A1.

XX 06-AUG-1998.

XX 05-FEB-1998;

XX 23-MAY-1997;

XX 05-FEB-1997;

PR 28-APR-1997; 97US-0847910.

XX (UYO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron AC;

XX WPI, 1998-437444/37.

XX N-PEDB; AAW45818.

PT Transgenic animals with gene for growth differentiation factor-8
PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease

XX Example 9; Fig 14b; 125pp; English.

XX This is the amino acid sequence of bovine growth differentiation
XX factor-8 (GDF-8), a novel member of the transforming growth factor-
XX beta superfamily that appears to relate to various cell
XX proliferative disorders especially those involving muscle, nerve
XX and adipose tissue. The sequence was deduced from a cDNA clone
XX (see AAW45818) isolated from a skeletal muscle cDNA library. The
XX invention provides novel mammalian and avian GDF-8 proteins (see
XX AAW69883-92). A transgenic non-human animal is claimed in which
XX GDF-8 expression is disrupted or interfered with. Also claimed
XX are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
XX from these animals; (2) method for increasing muscle mass in
XX animals by administering an antibody (Ab) that binds to GDF-8; (3)
XX inhibiting the action of GDF-8 by treating foetal or adult muscle
XX or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
XX acid encoding a GDF-8 protein truncated by loss of the C-terminal
XX active fragment. The transgenic animals have increased muscle mass
XX and for poultry reduced cholesterol contents. Method (3) is used
XX to treat muscle wasting or neuromuscular diseases, muscular atrophy
XX and aging, particularly muscular dystrophy, spinal cord or
XX traumatic injuries, congestive or obstructive lung disease, AIDS
XX and cachexia. Method (4) is used to treat cancer of muscle,
XX connective tissue and bone, or obesity. Also (not claimed) GDF-8
XX can be used to maintain myoblasts intended for transplanting or to
XX improve efficiency of fusion. Ab can be used to detect and
XX quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
XX also for immunotherapy and in vivo imaging.

XX Sequence 375 AA;

Query Match 100.0%; Score 630; DB 19; Length 375;

Best local similarity 100.0%; Pred. No. 6, 7e-59;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTSRCCRYPLTVDFEAFGMDWIAPKRYKANYSGCEPEFLQKYPHTL 60
DB 267 DFGLDDEHSTSRCCRYPLTVDFEAFGMDWIAPKRYKANYSGCEPEFLQKYPHTL 326

OY 61 VHQNPRGSGAGPCCPTPKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHQNPRGSGAGPCCPTPKSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 3

AAV33934 standard; peptide; 375 AA.

XX AAV33934;

XX 09-NOV-1999 (first entry)

XX Amino acid sequence of bovine myostatin.

XX Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick;

XX turkey; zebrafish; immune response; vaccine; body weight; muscle mass;

XX mammary gland tissue; lactation; feed uptake; muscle degeneration; GDF11.

XX Bos sp.

XX PN MO9942573-A1.
 XX PD 26-AUG-1999.
 XX PF 19-FEB-1999; 99MO-CA00128.
 XX PR 19-FEB-1998; 98US-0075213.
 XX PA (BIOS-) BIOSTAR INC.
 XX PI Barker CA, Morsey M;
 XX DR WPI; 1999-527471/44.
 XX PT New myostatin peptide, multimers and immunoconjugates for eliciting
 XX an immune response in a vertebrate against a myostatin immunogen
 XX PS Claim 4; Fig 1A-D; 109pp; English.

CC The invention provides myostatin peptides consisting of 3-100 amino
 CC acids, derived from a region of mouse, rabbit, human, baboon, bovine,
 CC porcine, ovine, chick, turkey or zebrafish myostatin (see sequences
 CC AA93930-939). The myostatin peptides are derived preferably from a
 CC region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the
 CC above sequences. The peptides and the nucleic acids encoding the peptides
 CC are useful as vaccines for eliciting an immune response in a vertebrate
 CC against a myostatin immunogen. They result in increasing body weight,
 CC muscle mass, number and size of muscle cells, muscle strength, mammary
 CC gland tissue, lactation, appetite or feed uptake, life span of the
 CC vertebrate, and cause a reduction in body fat content, useful for muscle
 CC wasting conditions. The vaccines are also useful for treating a disorder
 CC which comprises degeneration or wasting of muscle in a vertebrate, and
 CC useful for modulating GDP11 activity. The present sequence represents
 CC a bovine myostatin sequence.

XX SQ Sequence 375 AA;
 XX

Query Match 100.0%; Score 630; DB 20; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEEFVFLQKYPHTL 60
 DB 267 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEEFVFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGSGQIIYGIKIPAMVVDRCGS 109
 DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGSGQIIYGIKIPAMVVDRCGS 375

RESULT 4
 ID AA939317 standard; Protein; 375 AA.
 XX AA939317;
 AC
 XX
 AC
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE Bovine myostatin sequence.
 XX
 KM Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick;
 KM turkey; zebrafish; immune response; vaccine; body weight; muscle mass;
 KM mammary gland tissue; lactation; feed uptake; muscle degeneration;
 KM GDP11 activity.
 XX
 OS Bos sp.
 XX
 XX
 FH Key Location/Qualifiers
 FT 263..266
 FT "proteolytic cleavage site"
 FT 264..375
 FT /note="myostatin active region"

XX PN MO9942573-A1.
 XX PD 26-AUG-1999.
 XX PF 19-FEB-1999; 99MO-CA00128.
 XX PR 19-FEB-1998; 98US-0075213.
 XX PA (BIOS-) BIOSTAR INC.
 XX PI Barker CA, Morsey M;
 XX DR WPI; 1999-527471/44.
 XX DR N-PSDB; AA939349.
 XX PT New myostatin peptide, multimers and immunoconjugates for eliciting
 XX an immune response in a vertebrate against a myostatin immunogen
 XX PS Disclosure; Fig 16B; 109pp; English.

CC The invention provides myostatin peptides consisting of 3-100 amino
 CC acids, derived from a region of mouse, rabbit, human, baboon, bovine,
 CC porcine, ovine, chick, turkey or zebrafish myostatin (see sequences
 CC AA93930-939). The myostatin peptides are derived preferably from a
 CC region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the
 CC above sequences. The peptides and the nucleic acids encoding the peptides
 CC are useful as vaccines for eliciting an immune response in a vertebrate
 CC against a myostatin immunogen. They result in increasing body weight,
 CC muscle mass, number and size of muscle cells, muscle strength, mammary
 CC gland tissue, lactation, appetite or feed uptake, life span of the
 CC vertebrate, and cause a reduction in body fat content, useful for muscle
 CC wasting conditions. The vaccines are also useful for treating a disorder
 CC which comprises degeneration or wasting of muscle in a vertebrate, and
 CC useful for modulating GDP11 activity. The present sequence represents
 CC the amino acid sequence of bovine myostatin.

XX SQ Sequence 375 AA;
 XX

Query Match 100.0%; Score 630; DB 20; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEEFVFLQKYPHTL 60
 DB 267 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEEFVFLQKYPHTL 326
 QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGSGQIIYGIKIPAMVVDRCGS 109
 DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGSGQIIYGIKIPAMVVDRCGS 375

RESULT 5
 ID AA931191 standard; Protein; 375 AA.
 XX AA931191;
 AC
 XX
 AC
 XX
 DT 29-OCT-1999 (first entry)
 XX
 DE Bovine GDF-8 protein.
 XX
 KM GDF-8; growth differentiation factor receptor; GDF-11; therapy; human;
 KM veterinary; medicine; treatment; muscle tissue disease; wasting disease;
 KM neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat;
 KM traumatic injury; acquired immune deficiency syndrome; cachexia; bovine;
 KM congenital obstructive pulmonary disease; transgenic animal; transgene;
 KM food animal; cholesterol; muscle mass; diagnostic.
 XX
 OS Bos taurus.
 XX
 XX
 FH Key Location/Qualifiers
 FT 263..266
 FT "proteolytic cleavage site"
 FT 264..375
 FT /note="myostatin active region"

PD 11-FEB-1999.
 XX
 PF 28-JUL-1998; 98MO-US15598.
 XX
 PR 01-AUG-1997; 97US-0054461.
 XX
 PA (UYJO) UNITV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Lee S, McPherson A;
 XX
 DR WPI; 1999-153789/13.
 DR N-PSDB; AA209367.
 XX
 PT Recombinant cells that express growth-differentiation factor
 PT receptors - and related antibodies; nucleic acids; vector
 PT transformed cells; peptide fragments and transgenic animals; for
 PT treatment and diagnosis of muscle tissue diseases
 PS
 XX Examples; Fig 2b; 89pp; English.
 CC This invention describes novel recombinant cell lines that express
 CC growth-differentiation factor-8 (GDF-8) receptor polypeptide or GDF-11
 CC receptor polypeptide. The GDF receptors are used to identify specific
 CC (ant)agonists, potentially useful therapeutically in human or veterinary
 CC medicine. Antibodies derived from the products of the invention are used
 CC to treat muscle tissue diseases (particularly wasting diseases,
 CC neuromuscular disorders, muscular atrophy and aging, e.g. spinal cord and
 CC traumatic injury, congenital obstructive pulmonary diseases, acquired
 CC immune deficiency syndrome and cachexia). Transgenic, non-human animals
 CC that express the products of the invention from a transgene present in
 CC germ and somatic cells, specifically where GDF-8 receptor is expressed,
 CC may be food animals and have decreased fat and cholesterol contents and
 CC increased muscle mass. Peptides derived from the products of the
 CC invention and GDF-receptor binding and blocking agents, are reagents and
 CC diagnostic agents for studying muscle wasting diseases and for
 CC development of therapeutic agents. This sequence represents the bovine
 CC GDF-8 protein which is used in the method of the invention.
 CC
 SQ Sequence 375 AA;
 XX
 Query Match 100.0%; Score 630; DB 20; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDDEHSTSRCCRYPLTVDFEAFGMDMILAPRYRANCSGECFVPLQKYPTHL 60
 DB 267 DFGDGDDEHSTSRCCRYPLTVDFEAFGMDMILAPRYRANCSGECFVPLQKYPTHL 326
 QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGOIIYKIRPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGOIIYKIRPAMVVDRCGCS 375
 RESULT 6
 AAB20135
 ID AAB20135 standard; Protein; 375 AA.
 AC
 XX AAB20135;
 AC
 DT 30-APR-2001 (first entry)
 XX
 DE Cattle growth differentiation factor 8.
 KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
 KW vaccine; muscle; meat; cachexia; cardiac; cattle.
 KW
 OS Bos taurus.
 XX
 XX
 PN WO200105820-A2.
 PD 25-JUN-2001.
 XX
 PF 20-JUL-2000; 2000MO-DK00413.

XX
 XX 20-JUL-1999; 99DK-0001014.
 PR 26-JUL-1999; 99US-0145275.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Halkier T, Mouritsen S, Klyse S;
 XX
 DR WPI; 2001-112680/12.
 XX
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 PS
 XX Example 1; Page 82-83; 110pp; English.
 CC The present sequence is that of cattle growth differentiation factor
 CC 8 (GDF-8), also called myostatin. It is an object of the invention
 CC to produce a recombinant therapeutic vaccine capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
 CC provided that are capable of breaking autotolerance against
 CC autologous GDF-8. These comprise a C-terminal portion of human
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
 CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity is used to increase muscle mass by up to at least 45%
 CC in cattle, pigs and poultry used for meat production, reducing the
 CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used
 CC to treat human diseases such as cancer cachexia where muscle atrophy
 CC is pronounced and for patients suffering from acute and chronic
 CC heart failure.
 CC
 SQ Sequence 375 AA;
 XX
 Query Match 100.0%; Score 630; DB 22; Length 375;
 Best Local Similarity 100.0%; Pred. No. 6.7e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDDEHSTSRCCRYPLTVDFEAFGMDMILAPRYRANCSGECFVPLQKYPTHL 60
 DB 267 DFGDGDDEHSTSRCCRYPLTVDFEAFGMDMILAPRYRANCSGECFVPLQKYPTHL 326
 QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGOIIYKIRPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGOIIYKIRPAMVVDRCGCS 375
 RESULT 7
 AAE18664
 ID AAE18664 standard; Protein; 375 AA.
 AC
 XX AAE18664;
 AC
 DT 17-MAY-2002 (first entry)
 XX
 DE Bovine promyostatin.
 XX
 KW Bovine; promyostatin; myostatin; therapy; amyotrophic lateral sclerosis;
 KW neurodegenerative disease; GDF-11; muscular dystrophy; type II diabetes;
 KW muscle growth; myostatin prodomain; signal transduction; etherosclerosis;
 KW obesity; cachexia; hypertension; myocardial infarction; neuroprotective;
 KW muscular dystrophy; muscle wasting disorder; neuromuscular disorder;
 KW anorexia; growth differentiation factor; anorectic; immunomodulator;
 KW cardiac; metabolic.
 KW
 OS Bos sp.
 XX
 XX
 FH Key
 FT Domain
 FT
 FT Location/Qualifiers
 FT 20..262
 FT /note="Myostatin prodomain. This region is specifically
 FT claimed in claim 12 of the specification"

Region 267..374
/note="Mature myostatin. This region is specifically
claimed in claim 17 of the specification"

WO200209641-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US23510.

27-JUL-2000; 2000US-0628112.

(UYO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Lee S, McPherron AC;
WPI; 2002-179889/23.
N-PSDB; AAD29747.

Novel substantially purified promyostatin polypeptide portion
(myostatin prodomain or mature myostatin peptide), useful as myostatin
signal transduction modulator in muscle cell or adipose tissue, for
treating obesity -

Claim 5; Page 157-158; 175pp; English.

The present invention relates to a purified promyostatin polypeptide
portion. A myostatin peptide is useful as a target for treatment of
neurodegenerative diseases such as amyotrophic lateral sclerosis or
muscular dystrophy. A myostatin prodomain inhibits myostatin signal
transduction, while mature myostatin peptide referred as myostatin is
useful for inducing myostatin signal transduction by interacting
specifically with myostatin receptor expressed on the surface of the
cell. Modulating myostatin signal transduction is useful for regulating
skeletal muscle mass, where promyostatin portion is a negative regulator
or muscle growth. Modulating myostatin signal transduction in a muscle
cell or adipose tissue is useful for treating pathological conditions
associated with myostatin such as obesity and type II diabetes, cachexia,
conditions associated with obesity, e.g. atherosclerosis, hypertension,
myocardial infarction, muscle wasting disorders such as muscular
dystrophy, neuromuscular disorders, or anorexia. Myostatin prodomain is
useful for modulating the growth of muscle or adipose tissue in an
organism. Myostatin prodomain is useful for increasing muscle mass or
reducing fat content of an organism which is useful as a food source, and
myostatin peptide is useful for decreasing the growth of muscle tissue in
an organism e.g. an organism detrimental to an environment. Mutant
promyostatin which has dominant negative activity with respect to
myostatin or growth differentiation factor (GDF)-11 is useful for
reducing or inhibiting myostatin signal transduction. The present
sequence is bovine promyostatin.

Sequence 375 AA;

Query Match 100.0%; Score 630; DB 23; Length 375;
Best local similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCHDEHSTESRCRYPLTVDFEAFGMDWIAPRYKANYCGEGEFVLOKYPHTL 60
DB 267 DFGDCHDEHSTESRCRYPLTVDFEAFGMDWIAPRYKANYCGEGEFVLOKYPHTL 326

QY 61 VHOANPRGSAGPCCPTKMSPIINMLYFNGBGQIITGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTKMSPIINMLYFNGBGQIITGKIPAMVVDRCGCS 375

RESULT 8
AAU73625
ID AAU75625 standard; Protein; 375 AA.
AC AAU75625;
XX
DT 21-MAY-2002 (first entry)

Bovine promyostatin.

Bovine; promyostatin; immunomodulator; antidepressant; anorectic;
neuroprotective; antidiabetic; growth differentiation factor receptor;
myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;
wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
metabolic disorder; obesity; type II diabetes.

Bos sp.

WO200210214-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US23515.

27-JUL-2000; 2000US-0626896.

(UYO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

Lee S, McPherron AC;
WPI; 2002-217116/27.
N-PSDB; ABR15398.

New growth differentiation factor (GDF) receptors and modulators.
Useful for ameliorating wasting disorders such as cachexia, muscular
dystrophy or neuromuscular disease or a metabolic disorder such as
obesity or type II diabetes -

Claim 22; Fig 1; 184p; English.

The invention relates to a substantially purified growth differentiation
factor (GDF) receptor, specifically a myostatin receptor, or its
functional peptide portion. Also described is a method of modulating an
effect of myostatin on a cell by contacting the cell with an agent that
affects myostatin signal transduction in the cell. The method and the
receptor are useful for ameliorating the severity of a pathological
condition characterized by an abnormal amount, development or metabolic
activity of muscle or adipose tissue in a subject, particularly a wasting
disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular
disease) or a metabolic disorder (e.g. obesity or type II diabetes). The
present sequence represents the amino acid sequence of bovine
promyostatin.

Sequence 375 AA;

Query Match 100.0%; Score 630; DB 23; Length 375;
Best local similarity 100.0%; Pred. No. 6.7e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCHDEHSTESRCRYPLTVDFEAFGMDWIAPRYKANYCGEGEFVLOKYPHTL 60
DB 267 DFGDCHDEHSTESRCRYPLTVDFEAFGMDWIAPRYKANYCGEGEFVLOKYPHTL 326

QY 61 VHOANPRGSAGPCCPTKMSPIINMLYFNGBGQIITGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTKMSPIINMLYFNGBGQIITGKIPAMVVDRCGCS 375

RESULT 9
AAW97884
ID AAW97884 standard; Protein; 375 AA.
AC AAW97884;
XX
DT 07-JUN-1999 (first entry)
XX Bovine myostatin.
XX Myostatin; cattle; bovine; transforming growth factor beta;
KM double muscling; muscle hyperplasia; transgenic animal.

XX Bos taurus.
 OS
 XX MO9902667-A1.
 XX
 XX 21-JAN-1999.
 XX
 XX 14-JUL-1998; 98WO-IB01197.
 XX
 XX 15-JAN-1998; 98US-0007761.
 XX 14-JUL-1997; 97US-0891789.
 XX
 XX (UWIL-) UNIV LIEGE.
 XX
 XX Georges M, Grobet L, Poncet D;
 DR WPI, 1999-120869/10.
 DR N-PSDB; AAX24415, AAX24464.
 PT Increasing muscle mass in mammals - by decreasing myostatin
 PT expression
 XX
 XX Claim 19; Page 55; 75pp; English.
 XX
 CC This is the amino acid sequence of bovine myostatin, a member of
 CC the transforming growth factor beta superfamily, as encoded by the
 CC wild-type gene (see AAX24415). A mutation of this gene (see AAX24416)
 CC has been detected in cattle. Cattle of the Belgian Blue breed
 CC homozygous for the mutant gene are double-muscled. A new method of
 CC increasing muscle mass of a mammal having myostatin-expressing
 CC muscle cells, comprises administration of a nucleic acid molecule
 CC substantially complementary to at least a portion of mRNA
 CC encoding myostatin and of sufficient length to reduce myostatin
 CC expression and thus increase muscle mass. A ribozyme may also be
 CC used. Also claimed are: a method for determining muscular
 CC hyperplasia (MH) in a mammal using primers based upstream and
 CC downstream of the mutation; a diagnostic kit for determining
 CC the genotype of a sample of genetic material; a method for
 CC determining MH in a mammal; a method for determining double
 CC muscling in a bovine animal; a method for determining the myostatin
 CC genotype of an animal; a probe based on the myostatin gene
 CC a microbial host cell; a probe based on the myostatin gene
 CC mutation; transgenic mammals having MH phenotype; a myostatin
 CC knockout animal; and a transgenic bovine having a gene encoding
 CC active myostatin, and a heterologous nucleotide sequence antisense
 CC to that gene, and optionally further containing a gene encoding a
 CC nucleic acid sequence with ribozyme activity in transcriptional
 CC association with the antisense sequence.
 CC
 SQ Sequence 375 AA;
 Query Match 99.0%; Score 624; DB 20; Length 375;
 Best Local Similarity 99.1%; Pred. No. 2.9e-58;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYSGCEFEVFLQKYPHTL 60
 DB 267 DFGDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYSGCEFEVFLQKYPHTL 326
 QY 61 VHOANPRGASGPCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
 DB 327 VHOANPRASAGPCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375
 RESULT 10
 ID AAB20141
 XX AAB20141 standard; Protein; 109 AA.
 AC AAB20141;
 XX
 DT 30-APR-2001 (first entry)
 XX
 XX Human growth differentiation factor 8 C-terminal region.

XX Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
 KM vaccine; muscle; meat; cachexia; cardiatic; human; mutant; mutein.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX WO200105820-A2.
 XX
 XX 25-JAN-2001.
 XX
 XX 20-JUL-2000; 2000WO-DK00413.
 XX
 XX 20-JUL-1999; 99DK-0001014.
 XX 26-JUL-1999; 99US-0145275.
 XX
 XX (MEBI-) M & E BIOTECH AS.
 XX
 XX Halkier T, Mouritsen S, Klynsner S;
 DR WPI, 2001-112680/12.
 XX
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 PT
 PS Claim 17; Page 93-94; 110pp; English.
 XX
 CC The present sequence comprises the 109 amino acid residue
 CC C-terminal region of human growth differentiation factor 8
 CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
 CC AAX20131). The homodimer of this region is thought to be the
 CC biologically active form of GDF-8. It is an object of the
 CC invention to produce a recombinant therapeutic vaccine capable of
 CC effecting down-regulation of GDF-8 in order to increase the muscle
 CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
 CC are provided that are capable of breaking autotolerance against
 CC autologous GDF-8. These comprise the C-terminal portion of human
 CC GDF-8 in which a portion of the native sequence is replaced by a
 CC P2 or P30. The high number (9) of Cys residues in the C-terminal
 CC region limits the possible sites in which the T-cell epitope can be
 CC positioned without major disturbance of the native 3-dimensional
 CC structure of the protein. Nucleic acids encoding the GDF-8 variants
 CC can be used for genetic immunisation of the animals. Down-regulation
 CC of GDF-8 activity can increase muscle mass by up to at least 45% in
 CC cattle, pigs and poultry used for meat production, reducing the need
 CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 CC
 SQ Sequence 109 AA;
 Query Match 98.1%; Score 618; DB 22; Length 109;
 Best Local Similarity 98.2%; Pred. No. 3.4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYSGCEFEVFLQKYPHTL 60
 DB 1 DFGDDEHSTESRCRCRPLTVDFEAFGMDWIIAPKRYKANYSGCEFEVFLQKYPHTL 60
 QY 61 VHOANPRGASGPCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
 DB 61 VHOANPRGASGPCCTPTKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
 RESULT 11
 ID AAM51935
 XX AAM51935 standard; Protein; 109 AA.
 AC AAM51935;
 XX

DT 01-FEB-2002 (first entry)
 XX Human TGFbeta protein superfamily protein GDF8.
 DE
 XX
 XX Human; TGFbeta; transforming growth factor beta; mutant; antagonist;
 KW agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;
 KW formation; fibrosis; cirrhosis; osteoporosis; antipsoriatic;
 KW antifibrotic; hepatotropic; vulnary; GDF8.
 XX
 OS Homo sapiens.
 XX
 PN DE10026713-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 30-MAY-2000; 2000DE-1026713.
 XX
 PR 30-MAY-2000; 2000DE-1026713.
 XX
 PA (SEBALD) SEBALD W.
 XX
 PI Sebald W, Nickel J;
 XX WPI; 2002-042559/06.
 DR
 XX
 PT New mutain of transforming growth factor-beta superfamily protein,
 PT useful for treating or preventing e.g. ectopic bone formation, competes
 PT for receptor binding -
 XX
 PS Disclosure; Fig 6; 54pp; German.
 XX
 CC The present invention relates to mutains of a chain of a protein which,
 CC when in the form of a homodimer, has antagonistic or partial agonistic
 CC activity, and where the mutation results in the protein binding with low
 CC affinity to its receptor. The protein is a member of the transforming
 CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
 CC invention can be used in the treatment of diseases associated with the
 CC overexpression of TGFbeta family proteins, including ectopic bone
 CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
 CC cirrhosis. The present sequence is the human GDF8 protein.
 CC
 SQ Sequence 109 AA;
 Query Match 98.1%; Score 618; DB 23; Length 109;
 Best Local Similarity 98.2%; Pred. No. 3.4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGECEFVFLQKYPHTL 60
 DB 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGECEFVFLQKYPHTL 60
 OY 61 VHQANPRGSAAGCCTPTKMSPINMLYENGEGQIYVKIIPAMVVDRCGCS 109
 DB 61 VHQANPRGSAAGCCTPTKMSPINMLYENGEGQIYVKIIPAMVVDRCGCS 109
 RESULT 12
 AAR63161
 ID AAR63161 standard; Protein; 126 AA.
 AC AAR63161;
 DT 23-JUN-1995 (first entry)
 XX
 XX Mouse growth differentiation factor-8 partial sequence.
 DE
 XX
 KW Growth differentiation factor-8; GDF-8; cell proliferation;
 KW adipocyte; obesity; transforming growth factor-beta.
 XX
 OS Mus musculus.
 XX
 PN W09421681-A.
 FI

PD 29-SEP-1994.
 XX
 PF 18-MAR-1994; 94WO-US03019.
 XX
 PR 19-MAR-1993; 93US-0033923.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 XX
 PI Lee S, McPherron AC;
 XX WPI; 1994-316943/39.
 DR Q-PSDB; Q76380.
 XX
 PT New growth differentiation factor 8 - useful for treatment and
 PT diagnosis of cell proliferative disorders esp. of muscle.
 XX
 PS Disclosure; Page 41; 84pp; English.
 XX
 CC GDF-8 can be used to maintain cells before transplantation; to
 CC improve efficiency of cell fusion and to treat obesity or diseases
 CC related to abnormal adipocyte proliferation.
 CC
 SQ Sequence 126 AA;
 Query Match 98.1%; Score 618; DB 15; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGECEFVFLQKYPHTL 60
 DB 18 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGECEFVFLQKYPHTL 77
 OY 61 VHQANPRGSAAGCCTPTKMSPINMLYENGEGQIYVKIIPAMVVDRCGCS 109
 DB 78 VHQANPRGSAAGCCTPTKMSPINMLYENGEGQIYVKIIPAMVVDRCGCS 126
 RESULT 13
 AAM69883
 ID AAM69883 standard; Protein; 126 AA.
 AC AAM69883;
 XX
 XX
 DT 07-DEC-1998 (first entry)
 DE
 XX
 KW Murine growth differentiation factor-8 C-terminal fragment.
 KW
 KW Growth differentiation factor-8; GDF-8; mouse; transgenic animal;
 KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
 KW therapy.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 13..14
 FT Cleavage-site 16..17
 FT Protein 17..126
 FT /note="mature polypeptide"
 XX
 PN W09833887-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 05-FEB-1998; 98WO-US02479.
 XX
 PR 23-MAY-1997; 97US-0862445.
 PR 05-FEB-1997; 97US-0795071.
 PR 28-APR-1997; 97US-0847910.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Lee S, McPherron AC;

XX WPI: 1998-437444/37.
 DR N-PSDB; AA45809.
 XX Transgenic animals with gene for growth differentiation factor-8
 PT disrupted have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 2; Page 58; 125pp; English.
 XX This is the amino acid sequence of the C-terminal portion of mouse
 CC growth differentiation factor-8 (GDF-8), a novel member of the
 CC transforming growth factor-beta superfamily that appears to relate
 CC to various cell proliferative disorders, especially those involving
 CC muscle, nerve and adipose tissue. The sequence was deduced from a
 CC partial genomic clone (see AA45809). A full-length sequence (see
 CC AA45809) has been deduced from a cDNA clone (see AA42113). The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AA69883-92). A transgenic non-human animal is claimed in which
 CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle.
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.
 XX
 SQ Sequence 126 AA;
 Query Match 98.1%; Score 618; DB 19; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTESRCRRYPITVDFEAFGMDWIIAPKRYKANCSEGEFVLQKYPHTL 60
 DB 18 DFGDDEHSTESRCRRYPITVDFEAFGMDWIIAPKRYKANCSEGEFVLQKYPHTL 77
 QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGQIIYKIKIPAMVVDRCGCS 109
 DB 78 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGQIIYKIKIPAMVVDRCGCS 126
 RESULT 14
 ID AAY15386 standard; Protein: 126 AA.
 AC AAY15386;
 XX
 DT 08-DEC-1999 (first entry)
 XX
 DE C-terminal region of mouse Growth Differentiation Factor-8 (GDF-8).
 XX
 KW growth differentiation factor; tissue growth; muscle growth;
 KW cell differentiation; animal feed; muscle disorder;
 KW bone degeneration; nerve degeneration; GDF-8; development;
 KW transforming growth factor beta; TGF-beta.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 13..14

FT /label= Potential_proteolytic_cleavage_site
 FT 16..17 /label= Potential_proteolytic_cleavage_site
 FT /note= "Cleavage generates mature protein"
 EN W09940181-A1.
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99WO-US02511.
 XX
 PR 28-JUN-1998; 98US-0124180.
 PR 05-FEB-1998; 98US-0019070.
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Lee S, McPherron AC;
 XX
 DR WPI: 1999-494289/41.
 DR N-PSDB; AA206446.
 XX
 PT New differentiation factor useful for treating neurodegenerative
 PT diseases
 PS Example 2; Fig 2a; 138pp; English.
 XX
 CC This is the amino acid sequence of the C-terminal region of the GDF-8
 CC precursor protein. The predicted GDF-8 sequence contains two potential
 CC proteolytic processing sites.
 CC Cleavage of the precursor at the second of these sites would generate
 CC a mature C terminal fragment 109 amino acids in length with a predicted
 CC molecular weight of 12,400.
 CC GDF-8 has been shown to result in increased bone and muscle mass (such
 CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
 CC animals and forms of animal feed that can inhibit/reduce production of
 CC GDF-8 are of commercial interest.
 CC GDF-8 expression may also have a role in the therapy of abnormal growth
 CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
 CC antisense molecule or dominant negative polypeptide could be used with
 CC foetal or adult muscle cells, bone cells or progenitor cells. These
 CC agents can be administered to a patient suffering from a disorder such
 CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,
 CC osteoporosis, bone degenerative diseases, obesity or other adipocyte
 CC cell disorders, and aging for example.
 XX
 SQ Sequence 126 AA;
 Query Match 98.1%; Score 618; DB 20; Length 126;
 Best Local Similarity 98.2%; Pred. No. 4e-58;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTESRCRRYPITVDFEAFGMDWIIAPKRYKANCSEGEFVLQKYPHTL 60
 DB 18 DFGDDEHSTESRCRRYPITVDFEAFGMDWIIAPKRYKANCSEGEFVLQKYPHTL 77
 QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGQIIYKIKIPAMVVDRCGCS 109
 DB 78 VHOANPRGSAGPCCTPTKMSPINMLYFNGSGQIIYKIKIPAMVVDRCGCS 126
 RESULT 15
 ID AAB73182 standard; Protein: 126 AA.
 AC AAB73182;
 XX
 DT 11-MAY-2001 (first entry)
 XX
 DE Murine GDF-8 #1.
 XX
 KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KW muscular dystrophy; musculodegenerative disease; tissue repair;

KM muscle wasting disease; neuromuscular disorder; spinal cord injury;
 KW traumatic injury; congestive obstructive pulmonary disease.

OS Mus sp.

PN WO200112777-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22884.

PR 19-AUG-1999; 99US-0378238.

PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

XX WPI; 2001-211209/21.

DR N-PSDB; AAF63547.

PT New substantially purified growth differentiation factor-8 polypeptide,
 PT useful for treating muscle wasting disease, obesity, muscular
 PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
 PT and cachexia -

PS Example 2; Fig 2; 124pp; English.

CC The present invention relates to growth differentiation factor-8 (GDF-8)
 CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musculosclerotic diseases or in tissue repair due
 CC to trauma, obesity and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.

XX Sequence 126 AA;

Query Match 98.1%; Score 618; DB 22; Length 126;

Best Local Similarity 98.2%; Pred. No. 4e-58; 1; Indels 0; Gaps 0;

Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCGECFVFLQKYPHTL 60

DB 18 DFGIDCDHSTESRCRYPLTVDFEAFGMDWIAPKRYKANYCGECFVFLQKYPHTL 77

QY 61 VHOANPRGSAGPCPTPTKSPINMLYFNGEGQIYGYKIPAMVVDRCGS 109

DB 78 VHOANPRGSAGPCPTPTKSPINMLYFNGEGQIYGYKIPAMVVDRCGS 126

Search completed: January 31, 2003, 18:20:11
 Job time : 33 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2003, 18:20:18 ; Search time 8 Seconds

(without alignments)
274.933 Million cell updates/sec

Title: US-09-620-586b-12

Perfect score: 630

Sequence: 1 DFGIDDEHSTSRCCRYPL.....EQGIYGRIPAMVDRGCS 109

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 122226 seqs, 2017851 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database:

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	375	9	US-09-841-730-12
2	630	100.0	375	9	US-09-859-211-21
3	618	98.1	126	9	US-09-859-211-6
4	618	98.1	130	9	US-09-859-211-33
5	618	98.1	226	9	US-09-859-211-35
6	618	98.1	374	9	US-09-841-730-8
7	618	98.1	375	9	US-09-841-730-2
8	618	98.1	375	9	US-09-841-730-14
9	618	98.1	375	9	US-09-841-730-18
10	618	98.1	375	9	US-09-859-211-14
11	618	98.1	375	9	US-09-859-211-23
12	618	98.1	375	9	US-09-859-211-27
13	618	98.1	375	9	US-09-859-211-29
14	618	98.1	376	10	US-09-454-440-5
15	618	98.1	376	9	US-09-841-730-4
16	618	98.1	376	9	US-09-841-730-6
17	618	98.1	376	9	US-09-859-211-12
18	618	98.1	376	9	US-09-859-211-25
19	618	98.1	376	9	US-09-813-398-38

20	618	98.1	376	10	US-09-859-894A-11	Sequence 11, Appl
21	618	97.3	375	9	US-09-859-894A-5	Sequence 10, Appl
22	612	97.1	375	9	US-09-841-730-10	Sequence 10, Appl
23	612	97.1	375	9	US-09-859-211-19	Sequence 15, Appl
24	611	97.0	109	10	US-09-754-826-2	Sequence 2, Appl
25	608	96.5	375	9	US-09-841-730-16	Sequence 16, Appl
26	608	96.5	375	9	US-09-859-211-31	Sequence 11, Appl
27	579	91.9	108	9	US-09-859-211-8	Sequence 4, Appl
28	579	91.0	126	10	US-09-454-540-1	Sequence 4, Appl
29	573	91.0	126	10	US-09-859-894A-4	Sequence 25, Appl
30	573	91.0	407	9	US-09-841-730-25	Sequence 25, Appl
31	573	91.0	407	10	US-09-454-540-2	Sequence 2, Appl
32	573	91.0	407	10	US-09-454-540-6	Sequence 6, Appl
33	573	91.0	407	10	US-09-859-894A-2	Sequence 20, Appl
34	573	91.0	408	9	US-09-813-398-13	Sequence 33, Appl
35	559	88.7	374	9	US-09-841-730-20	Sequence 20, Appl
36	553	87.8	136	9	US-09-841-730-29	Sequence 29, Appl
37	553	87.8	157	9	US-09-841-730-27	Sequence 27, Appl
38	504.5	80.1	128	10	US-09-205-659-317	Sequence 317, App
39	245	38.9	120	10	US-09-813-459-20	Sequence 20, Appl
40	245	38.9	120	12	US-10-115-406-20	Sequence 20, Appl
41	245	38.9	121	9	US-09-859-211-46	Sequence 46, Appl
42	245	38.9	121	9	US-09-880-708-24	Sequence 24, Appl
43	245	38.9	408	9	US-09-813-398-26	Sequence 26, Appl
44	245	38.9	408	9	US-09-813-398-22	Sequence 22, Appl
45	232.5	36.9	118	12	US-10-115-406-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-841-730-12
; Sequence 12, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS.
; FILE REFERENCE: JH01470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIOR APPLICATION NUMBER: 2001-04-24
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Bovine

Query Match 100.0%; Score 630; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 7.2e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDDEHSTSRCCRYPLVNDPEAFGMDWIIAPKRYKAYSGSGEPEVFLQKPHHL 60
DB 267 DFGIDDEHSTSRCCRYPLVNDPEAFGMDWIIAPKRYKAYSGSGEPEVFLQKPHHL 326
QY 61 VQANRPGSAGCCPTMGSRIMKLYNGEGQIYGRIPAMVDRGCS 109
DB 327 VQANRPGSAGCCPTMGSRIMKLYNGEGQIYGRIPAMVDRGCS 375
RESULT 2

```
US-09-859-211-21
/ Sequence 21, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT APPLICATION NUMBER: US/09/859,211
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 375
/ TYPE: PRT
/ ORGANISM: Bovine
US-09-859-211-21

Query Match
Best Local Similarity 100.0%; Score 630; DB 9; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 60
DB 267 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 326
QY 61 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 109
DB 337 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 375

RESULT 3
US-09-859-211-6
/ Sequence 6, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT APPLICATION NUMBER: US/09/859,211
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
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/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-859-211-6

Query Match
Best Local Similarity 98.1%; Score 618; DB 9; Length 126;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 60
DB 18 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 77
QY 61 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 109
DB 78 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 126

RESULT 4
US-09-859-211-33
/ Sequence 33, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT APPLICATION NUMBER: US/09/859,211
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 130
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-859-211-33

Query Match
Best Local Similarity 98.1%; Score 618; DB 9; Length 130;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 60
DB 22 DFGDDCHSTSRCCRYPLTVDFEARGMDWIIAPRYKANYSGGCEFFVLOKYPHTL 81
QY 61 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 109
DB 82 VHQANPRGSAGPCCPTTKMSPINMLYFNGBGQIIYGIKIPAMVDRCCGS 130

RESULT 5
US-09-859-211-35
/ Sequence 35, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Se-Jin
/ APPLICANT: McPherron, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
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CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 226
TYPE: PRT
ORGANISM: Gallus gallus
US-09-859-211-35

Query Match 98.1%; Score 618; DB 9; Length 226;
Best Local Similarity 98.2%; Pred. No. 7, 8e-58;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 60
DB 118 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 177
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 109
DB 178 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 226

RESULT 5
US-09-841-730-8
Sequence 8, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 374
TYPE: PRT
ORGANISM: Gallus gallus
US-09-841-730-8

Query Match 98.1%; Score 618; DB 9; Length 374;
Best Local Similarity 98.2%; Pred. No. 1, 3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 60
DB 266 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 325

QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 109
DB 326 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 374

RESULT 7
US-09-841-730-2
Sequence 2, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-841-730-2

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1, 3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 60
DB 267 DFGDDCHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYSGCEFPVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPKMSPINMLYFNKGQIIYGIKIPAMVVDRCGCS 375

RESULT 8
US-09-841-730-14
Sequence 14, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 375
TYPE: PRT
ORGANISM: Porcine
US-09-841-730-14

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 375

RESULT 9
US-09-841-730-18
Sequence 18; Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JHU1470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 375
TYPE: PRT
ORGANISM: Meleagris gallopavo
US-09-841-730-18

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 375

RESULT 10
US-09-859-211-14
Sequence 14; Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071

PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-211-14

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 375

RESULT 11
US-09-859-211-23
Sequence 23; Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/144001
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 375
TYPE: PRT
ORGANISM: Gallus gallus
US-09-859-211-23

Query Match 98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYKGIIPAMVVDRCGCS 375

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RESULT 12
US-09-859-211-27
; Sequence 27, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Melagris gallopavo
US-09-859-211-27

Query Match          98.1%; Score 618; DB 9; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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US-09-859-211-29
; Sequence 29, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51

RESULT 13
US-09-859-211-29
; Sequence 29, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51

RESULT 14
US-09-454-540-5
; Sequence 5, Application US/09454540
; Patent No. US20010053358A1
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,540
; FILING DATE: 06-DEC-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HALL, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: GDP-8
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..375
; US-09-454-540-5

Query Match          98.1%; Score 618; DB 10; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 DFGIDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEVFLOKYPHTL 60
    |||||||
Db 267 DFGIDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYENGESQIIYGIKIPAMVVDRCGS 109
    |||||||
Db 327 VHOANPRGSAGPCCPTPKMSPINMLYENGESQIIYGIKIPAMVVDRCGS 375
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RESULT 15

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US-09-841-730-4
; Sequence 4, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherson, Alexandra C
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: J041470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-841-730-4
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Query Match 98.1%; Score 618; DB 9; Length 376;
Best Local Similarity 98.2%; Pred. No. 1.3e-57;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 DFGIDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEVFLOKYPHTL 60
    |||||||
Db 268 DFGIDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEVFLOKYPHTL 327
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYENGESQIIYGIKIPAMVVDRCGS 109
    |||||||
Db 328 VHOANPRGSAGPCCPTPKMSPINMLYENGESQIIYGIKIPAMVVDRCGS 376
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Search completed: January 31, 2003, 18:27:18
Job time : 8 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:19:03 (Search time 17.5 Seconds)

(Without alignments)
501.352 Million cell updates/sec

Title: US-09-620-586b-12

Perfect score: 630
Sequence: 1 DFGLDDEHSTESRCRYPL.....EGGIYKIPAMVVDRCGCS 109

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 402399 seqs, 80492318 residues

Total number of hits satisfying chosen parameters: 402399

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database:

Pending Patents: AA New:
1: /cgn2_6/prodata/2/paa/PCr NEW COMB. pep.*
2: /cgn2_6/prodata/2/paa/US06 NEW COMB. pep.*
3: /cgn2_6/prodata/2/paa/US07 NEW COMB. pep.*
4: /cgn2_6/prodata/2/paa/US08 NEW COMB. pep.*
5: /cgn2_6/prodata/2/paa/US09 NEW COMB. pep.*
6: /cgn2_6/prodata/2/paa/US10 NEW COMB. pep.*
7: /cgn2_6/prodata/2/paa/US00 NEW COMB. pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	109	5	US-09-620-586b-12
2	630	100.0	375	5	US-09-620-586b-5
3	630	100.0	375	6	US-10-251-115-2
4	618	98.1	109	5	US-09-620-586b-11
5	618	98.1	126	6	US-10-278-803-6
6	618	98.1	160	5	US-09-620-586b-23
7	618	98.1	254	5	US-09-620-586b-22
8	618	98.1	352	5	US-09-620-586b-2
9	618	98.1	375	5	US-09-871-604A-5
10	618	98.1	375	5	US-09-620-586b-1
11	618	98.1	375	5	US-09-620-586b-3
12	618	98.1	375	5	US-09-620-586b-8
13	618	98.1	375	6	US-10-278-803-14
14	618	98.1	375	6	US-10-278-803-19
15	618	98.1	375	6	US-10-278-803-21
16	618	98.1	375	6	US-10-278-803-23
17	618	98.1	375	6	US-10-278-803-27
18	618	98.1	375	6	US-10-251-115-8
19	618	98.1	375	6	US-10-335-483-14
20	618	98.1	376	5	US-09-871-604A-10
21	618	98.1	376	5	US-09-620-586b-4
22	618	98.1	376	5	US-09-620-586b-7
23	618	98.1	376	6	US-10-278-803-12
24	618	98.1	376	6	US-10-278-803-25
25	618	98.1	376	6	US-10-251-115-6
26	618	98.1	376	6	US-10-251-115-6

27	618	98.1	376	5	US-10-335-483-12	Sequence 12, App1
28	612	97.1	375	5	US-09-620-586b-10	Sequence 10, App1
29	608	96.5	375	5	US-09-620-586b-6	Sequence 6, App1
30	579	91.9	108	6	US-10-278-803-8	Sequence 8, App1
31	579	91.9	108	6	US-10-335-483-8	Sequence 8, App1
32	573	91.0	126	5	US-09-871-604A-4	Sequence 4, App1
33	573	91.0	405	5	US-09-871-604A-2	Sequence 4, App1
34	573	91.0	407	5	US-09-871-604A-2	Sequence 4, App1
35	559	88.7	109	5	US-09-620-586b-9	Sequence 9, App1
36	540	85.9	109	5	US-09-620-586b-17	Sequence 17, App1
37	522	82.9	109	5	US-09-620-586b-15	Sequence 15, App1
38	519	82.4	109	5	US-09-620-586b-21	Sequence 21, App1
39	518	82.2	109	5	US-09-620-586b-16	Sequence 16, App1
40	510	81.0	109	5	US-09-620-586b-20	Sequence 20, App1
41	504.5	80.1	128	5	US-09-963-693-317	Sequence 317, App1
42	494	78.4	109	5	US-09-620-586b-18	Sequence 18, App1
43	490	77.8	109	5	US-09-620-586b-19	Sequence 19, App1
44	258.5	41.0	102	6	US-10-072-012-831	Sequence 831, App1
45	258.5	41.0	102	6	US-10-072-012-833	Sequence 833, App1

ALIGNMENTS

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RESULT 1
US-09-620-586b-12
; Sequence 12, Application US/09620586b
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586b
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(109)
; OTHER INFORMATION: Identical to residues 267-375 in SEQ ID NO: 5
US-09-620-586b-12

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Query Match 100.0%; Score 630; DB 5; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.9e-63;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLOKYPHTL 60
Db 1 DFGLDDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEFFVLOKYPHTL 60
QY 61 VHQANPRGAGPCTPTKMSPIMLYFNGEGQIYKIPAMVVDRCGCS 109
Db 61 VHQANPRGAGPCTPTKMSPIMLYFNGEGQIYKIPAMVVDRCGCS 109

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RESULT 2
US-09-620-586b-5
; Sequence 5, Application US/09620586b
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586b
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Bos taurus

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US-09-620-586b-5

Query Match 100.0%; Score 630; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 109
DB 327 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 375

RESULT 3

US-10-251-115-2
Sequence 2, Application US/10251115
GENERAL INFORMATION:
APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique
TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMAL
FILE REFERENCE: 52836/00016
CURRENT APPLICATION NUMBER: US/10/251,115
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/482,573
PRIOR FILING DATE: 1997-07-14
PRIOR APPLICATION NUMBER: 06/891,789
PRIOR FILING DATE: 1997-07-14
PRIOR APPLICATION NUMBER: 09/007,761
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: PCT/IB98/01197
PRIOR FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Bos taurus
US-10-251-115-2

Query Match 100.0%; Score 630; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.3e-62;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 109
DB 327 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 375

RESULT 4

US-09-620-586b-11
Sequence 11, Application US/09620586B
GENERAL INFORMATION:
APPLICANT: Mee Biotech A/S
TITLE OF INVENTION: Method for down-regulating GDF-8 activity
FILE REFERENCE: 3631-0117P
CURRENT APPLICATION NUMBER: US/09/620,586B
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(109)
OTHER INFORMATION: Identical to residues 267-375 in SEQ ID NO: 1
US-09-620-586b-11

Query Match 98.1%; Score 618; DB 5; Length 109;
Best Local Similarity 98.2%; Pred. No. 2.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 60
DB 1 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 60

QY 61 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 109
DB 61 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 109

RESULT 5

US-10-278-803-6
Sequence 6, Application US/10278803
GENERAL INFORMATION:
APPLICANT: Se-Jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,803
FILING DATE: 22-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-Nov-1999
APPLICATION NUMBER: 08/795,071
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US94/03019
FILING DATE: 18-March-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hallie, Ph.D.
REGISTRATION NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-278-803-6

Query Match 98.1%; Score 618; DB 6; Length 126;
Best Local Similarity 98.2%; Pred. No. 2.5e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGDGDCHSTESRCCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPHTL 77

QY 61 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 109
DB 78 VHOANPRGSGAGPCTPTKMSPINMLYFNNGSOIITGKIIPANVVDRCGCS 126

RESULT 6
US-10-335-483-6
; Sequence 6, Application US/10335483
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; Lee, Se-jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,483
; FILING DATE: 31-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-335-483-6
Query Match 98.1%; Score 618; DB 6; Length 126;
Best Local Similarity 98.2%; Pred. No. 2,5e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 DFGDIDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANCSCGECFVFLQKYPHTL 60
Db 18 DFGDIDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANCSCGECFVFLQKYPHTL 77
Cy 61 VHQNPRGSAGPCTPTKMSPINMLYFNKGQIITGKIPAMVVDRCGCS 109
Db 78 VHQNPRGSAGPCTPTKMSPINMLYFNKGQIITGKIPAMVVDRCGCS 126
RESULT 7
US-09-620-586B-23
; Sequence 23, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&B Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23

LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (16)..(36)
; OTHER INFORMATION: Tetanus toxoid P30 epitope (SEQ ID NO: 14)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (37)..(51)
; OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 13)
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(15)
; OTHER INFORMATION: Identical to residues 216-230 of SEQ ID NO: 1
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (52)..(160)
; OTHER INFORMATION: Identical to residues 267-375 of SEQ ID NO: 1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Cys or Ser
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (141)..(142)
; OTHER INFORMATION: Lys Glu or Gln Gly
US-09-620-586B-23
Query Match 98.1%; Score 618; DB 5; Length 160;
Best Local Similarity 98.2%; Pred. No. 3.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 DFGDIDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANCSCGECFVFLQKYPHTL 60
Db 52 DFGDIDCEHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANCSCGECFVFLQKYPHTL 111
Cy 61 VHQNPRGSAGPCTPTKMSPINMLYFNKGQIITGKIPAMVVDRCGCS 109
Db 112 VHQNPRGSAGPCTPTKMSPINMLYFNKGQIITGKIPAMVVDRCGCS 160
RESULT 8
US-09-620-586B-22
; Sequence 22, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&B Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (110)..(124)
; OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 13)
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (125)..(145)
; OTHER INFORMATION: Diphtheria toxoid P30 epitope (SEQ ID NO: 14)
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(109)
; OTHER INFORMATION: 109 C-terminal residues of human and bovine GDF-8
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (146)..(254)

```

; OTHER INFORMATION: 109 C-terminal residues of human and bovine GDF-8
; OTHER INFORMATION: (residues 267-375 in SEQ ID NO: 1)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (90)..(91)
; OTHER INFORMATION: Lys Glu or Glu Gly
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (235)..(236)
; OTHER INFORMATION: Identical to (90)..(91)
US-09-620-586B-22

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Query Match          98.1%; Score 618; DB 5; Length 254;
Best Local Similarity 98.2%; Pred. No. 4,9e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 60
DB 146 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 205

```

```

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 206 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 254

```

```

RESULT 9
US-09-620-586B-2
; Sequence 2, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-09-620-586B-2

```

```

Query Match          98.1%; Score 618; DB 5; Length 362;
Best Local Similarity 98.2%; Pred. No. 6,9e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 60
DB 254 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 313

```

```

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 314 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 362

```

```

RESULT 10
US-09-871-604A-5
; Sequence 5, Application US/09871604A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: LEE, Se-jin
; APPLICANT: McPHERSON, Alexandra C.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN ANIMALS EXPRESSING A GDF-11 DOMINANT NEGATIVE
; FILE REFERENCE: JHU1200-10
; CURRENT APPLICATION NUMBER: US/09/871,604A
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: US 09/123,929
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: US 09/019,901
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: US 08/795,671
; PRIOR FILING DATE: 1997-02-06

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; PRIOR APPLICATION NUMBER: US 08/706,958
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: US 08/272,763
; PRIOR FILING DATE: 1994-07-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Human GDF-8
US-09-871-604A-5

```

```

Query Match          98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7,1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 60
DB 267 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 326

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```

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

```

```

RESULT 11
US-09-620-586B-1
; Sequence 1, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-586B-1

```

```

Query Match          98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7,1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 60
DB 267 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPTHLL 326

```

```

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS 375

```

```

RESULT 12
US-09-620-586B-3
; Sequence 3, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-620-586B-3

```

```

Query Match          98.1%; Score 618; DB 5; Length 375;

```

Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 60
Db 267 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 326

Qy 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 109
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 375

RESULT 13
US-09-620-586B-8
; Sequence 8, Application US/09620586B
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: Method for down-regulating GDF-8 activity
; FILE REFERENCE: 3631-0117P
; CURRENT APPLICATION NUMBER: US/09/620,586B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-620-586B-8

Query Match 98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 60
Db 267 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 326

Qy 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 109
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 375

RESULT 14
US-10-278-803-14
; Sequence 14, Application US/10278803
; GENERAL INFORMATION:
; APPLICANT: Se-jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.,
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: PASTESD for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,803
; FILING DATE: 22-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-Nov-1999
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match 98.1%; Score 618; DB 5; Length 375;
Best Local Similarity 98.2%; Pred. No. 7.1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 60
Db 267 DFGDDEHSTESRCRYPPLVDFEAFGMDWIIAPKRYKANYSGSGCEFFVLOKYPHTL 326

Qy 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 109
Db 327 VHOANPRGSAGPCCPTPTKMSPINMLYFNGBQIITYGKIPAMVVDRCGCS 375

RESULT 15
US-10-278-803-19
; Sequence 19, Application US/10278803
; GENERAL INFORMATION:
; APPLICANT: Se-jin Lee et al.,
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.,
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: PASTESD for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/278,803
; FILING DATE: 22-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,501
; FILING DATE: 30-Nov-1999
; APPLICATION NUMBER: 08/795,071
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/US94/03019
; FILING DATE: 18-March-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/105001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:

Sun Feb 2 11:34:36 2003

us-09-620-586b-12.rpn

CLONE: Baboon GDF-8

FEATURE:
NAME/KEY: Protein
LOCATION: 1...375
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-278-803-19

Query Match 98.1%; Score 618; DB 6; Length 375;

Best Local Similarity 98.2%; Pred. No. 7.1e-61; Mismatches 1; Indels 0; Gaps 0;

Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 60
DB 267 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGECFVFLQKYPHTL 326

QY 61 VHQANPRGSAGPCCPTPKMSPINMLYFNGSGQIIYGRKIPAMVVDRCGS 109
DB 327 VHQANPRGSAGPCCPTPKMSPINMLYFNGSGQIIYGRKIPAMVVDRCGS 375

Search completed: January 31, 2003, 18:26:55
Job time : 17.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 25 Seconds

(without alignments)
898,365 Million cell updates/sec

Title: US-09-620-586b-12

Sequence: 1 DFGDDEHSTSRRCRYPL.....EQGIYKIRAMVYDRGGS 109

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	375	6	Q8WNS6
2	618	98.1	162	6	Q9TSY2
3	618	98.1	375	6	Q9GWS7
4	618	98.1	375	6	Q95J86
5	618	98.1	375	13	Q8UMD8
6	618	98.1	375	13	Q8UMD7
7	612	97.3	375	13	Q985P0
8	612	97.3	375	13	Q8UMD9
9	595	94.4	185	6	Q95N11
10	595	94.4	185	6	Q95N11
11	588	93.3	185	13	Q90Y10
12	559	88.7	385	13	Q90W05
13	556	88.3	385	13	Q90W05
14	553	87.8	373	13	Q90ZD1
15	553	87.8	373	13	Q90ZD1
16	553	87.8	373	13	Q90ZD1

17	553	87.8	376	13	Q98TB4
18	553	87.8	376	13	Q90WC9
19	553	87.8	376	13	Q90WC9
20	552	87.6	373	13	Q90W17
21	551	87.5	376	13	Q90W06
22	548	87.0	373	13	Q98TB3
23	546	86.7	373	13	Q98TB3
24	543	86.2	359	13	Q9W759
25	532	84.4	359	13	Q8G553
26	521	82.7	107	6	Q9XG54
27	394	62.5	78	6	Q9XG56
28	311	49.4	191	13	Q98TY4
29	302	47.9	104	13	Q90Z79
30	299.5	47.5	598	5	Q94YF4
31	299.5	47.5	598	5	Q94YF4
32	286	45.4	38	6	Q95WF3
33	259	41.1	263	13	Q80H11
34	257	40.8	370	13	Q91350
35	245	38.9	395	13	Q9PWG6
36	244.5	38.8	115	13	Q9DGB9
37	244.5	38.8	393	13	Q90261
38	243.5	38.7	392	13	Q9PWR8
39	242.5	38.5	115	13	Q9PGF1
40	242.5	38.5	115	13	Q9DGF0
41	242.5	38.5	115	13	Q9DGB5
42	239.5	38.0	138	13	Q9WKT9
43	233.5	37.1	359	13	Q9YGV1
44	231.5	36.7	349	5	Q97J38
45	223.5	35.5	361	5	Q96504

ALIGNMENTS

RESULT 1

ID	Q8WNS6	PRELIMINARY:	PRT:	375 AA.
AC	Q8WNS6	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Myosardin.			
GN	GDF8.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Shibata M., Muramoto T., Aikawa K.;			
RT	"Genomic organization and sequence of the myosardin gene in bovine.";			
RL	Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AB076403; BAB79498.1; "			
DR	InterPro; IPR002048; EF-hand.			
DR	InterPro; IPR001839; TGFb.			
DR	InterPro; IPR001111; TGFb N.			
DR	Pfam; PF00019; TGF-beta; T.			
DR	Pfam; PF00688; TGFb propeptide; 1.			
DR	Pfam; PF000357; TGFb 1.			
DR	SMART; SM00204; TGFb; 1.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN.1.			
DR	PROSITE; PS00250; TGF_BETA_1; UNKNOWN.1.			
DR	SEQUENCE 375 AA; 42524 MW; 0EC27616C202F556 CRC64;			

Query Match 100.0%; Score 630; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.ee-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTSRRCRYPLTVDFEAFGMDWIIARPKYKAYGSGCEPFYLOKYPPTH 60
Db 267 DFGDDEHSTSRRCRYPLTVDFEAFGMDWIIARPKYKAYGSGCEPFYLOKYPPTH 326

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 2

Q9TSY2 PRELIMINARY; PRT; 162 AA.

AC Q9TSY2; 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE Myostatin (Fragment).
 GN MSTN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 NC NCB1_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20078370; PubMed=10612246;
 RA Stratiell A., Kopecky M.;
 RT "genomic organization, sequence and polymorphism of the porcine
 myostatin (GDF8; MSTN) gene";
 RL Anim. Genet. 30:468-470(1999).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AJ237920; CAB40844.1; -.
 DR HSSP; P18075; IEMP.
 DR InterPro; IPR002400; GF_cyknoc.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 FT NON TER 1
 SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;

Query Match 98.1%; Score 618; DB 6; Length 162;
 Best Local Similarity 98.2%; Pred. No. 2.8e-64;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 60
 DB 54 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 113
 QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 114 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 162

RESULT 3

Q9GM97 PRELIMINARY; PRT; 375 AA.

AC Q9GM97; 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DE Myostatin.
 GN MSTN.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NC NCB1_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=THROUGHERED;
 RA Hosoyama T., Tamaouchi K., Tojo H., Tachi C.;
 RT "Molecular cloning of equine myostatin cDNA and serum level of
 myostatin in horse";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AB033541; BAB16046.1; -.
 DR HSSP; P18075; IEMP.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb_1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBE84D9936 CRC64;

Query Match 98.1%; Score 618; DB 6; Length 375;
 Best Local Similarity 98.2%; Pred. No. 6.5e-64;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 60
 DB 267 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 326
 QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 4

Q95J86 PRELIMINARY; PRT; 375 AA.

AC Q95J86; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE Myostatin.
 GN Myostatin.
 OS Macaca fascicularis (Craab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 NC NCB1_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GASTROCNEMUS;
 RA Smock S.L., Owen T.A.;
 RT "Cloning of the open reading frame DNA for macaque fascicularis
 (cynomolgus macaque) myostatin (GDF8)";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC EMBL; AY055750; AAL17640.1; -.
 DR EMBL; AY055750; AAL17640.1; -.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb_N.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRODOM; PD000357; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SQ SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match 98.1%; Score 618; DB 6; Length 375;
 Best Local Similarity 98.2%; Pred. No. 6.5e-64;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 60
 DB 267 DFGDCCHESTBRCRCRPLTVDFAFGMDWITAPKRYKANYSGGCEPFVLOKYPHTL 326
 QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 5

Q8UMD8 PRELIMINARY; PRT; 375 AA.

AC Q8UMD8; 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 GN Myostatin.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 NCBI_TaxID=8932;

RN [1]

RP SEQUENCE FROM N.A.

RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
 RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
 Duck, Goose, Pigeon and Quail."
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF440863; AAL35277.1; -

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.

SQ PROSITE 375 AA; 42739 MW; 88296FOAE779476E CRC64;

Query Match

Best Local Similarity 98.2%; Score 618; DB 13; Length 375;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 60

DB 267 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 326

QY 61 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 109

DB 327 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 375

RESULT 6

Q8UMD7 PRELIMINARY; PRT; 375 AA.

AC Q8UMD7; 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 GN Myostatin.
 OS Columba livia (Domestic pigeon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Columbiformes; Columbidae; Columba.
 NCBI_TaxID=8932;

RN [1]

RP SEQUENCE FROM N.A.

RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
 RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
 Duck, Goose, Pigeon and Quail."
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF440864; AAL35278.1; -

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 SQ SEQUENCE 375 AA; 42721 MW; 89391AA42DE0725 CRC64;

Query Match 98.1%; Score 618; DB 13; Length 375;
 Best Local Similarity 97.2%; Pred. No. 2,56-63;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 60

DB 267 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 326

QY 61 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 109

DB 327 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 375

RESULT 7

Q98SP0 PRELIMINARY; PRT; 375 AA.

AC Q98SP0; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 GN Myostatin.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Columbiformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhang Y., Yang W., Zhu D.;
 RT "Genomic structure and expression of the chicken GDF-8 during
 development."
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL; AF346599; AAL18000.1; -

DR HSP; P18075; 1EMP.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFb; 1.

DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

DR GlycoProtein.

SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;

Query Match 97.3%; Score 613; DB 13; Length 375;
 Best Local Similarity 97.2%; Pred. No. 2,56-63;
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 60

DB 267 DGLDGDHSTESRCRRYPLTVDFEAFGMDWIIAPRYKANYCGSECFVFLQKYPHTL 326

QY 61 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 109

DB 327 VHOANPRGAGPCCPTPKMSPINMLYFNGEQIYYGKIPAMVVDRCGCS 375

RESULT 8

Q8UMD9 PRELIMINARY; PRT; 375 AA.

AC Q8UMD9; 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

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DE Myostatin.
GN MSTN.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
OX NCBI_TaxID=8943;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440862; AL35276.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR Prodom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42667 MW; 57DD849D3AA2978C CRC64;

Query Match 97.1%; Score 612; DB 13; Length 375;
Best Local Similarity 97.2%; Pred. No. 3.3e-63;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 109
DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 375

RESULT 9
Q8UWEO PRELIMINARY; PRT; 375 AA.
ID Q8UWEO;
AC Q8UWEO;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440861; AL35275.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR Prodom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGF-beta; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
SQ SEQUENCE 375 AA; 42817 MW; 1BA7FF5225C23620 CRC64;

Query Match 96.8%; Score 610; DB 13; Length 375;
Best Local Similarity 97.2%; Pred. No. 5.6e-63;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60

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DB 267 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 326

QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 109
DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 375

RESULT 10
Q95N11 PRELIMINARY; PRT; 185 AA.
ID Q95N11;
AC Q95N11;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in goat."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY032689; AA849790.1; -.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR Prodom; PD000357; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA_1; UNKNOWN_1.
KW Glycoprotein.
FT NON_TER 1
FT TER 185
SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match 94.4%; Score 595; DB 6; Length 185;
Best Local Similarity 95.3%; Pred. No. 1.5e-61;
Matches 102; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 79 DFGLDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 138

QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 107
DB 139 VHOANPRGSAGPCCTPTKMSPINMLYFNGEQIIVGKIIPAWVDRCG 185

RESULT 11
Q9WZ18 PRELIMINARY; PRT; 185 AA.
ID Q9WZ18;
AC Q9WZ18;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Myostatin (Fragment).
GN MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of Intron 2 of the myostatin gene in sheep."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF266758; AA78069.1; -.

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DR H5SP: P12643; 3BMP.
 DR InterPro: IPR001839; TGF β .
 DR InterPro: IPR001111; TGF β .N.
 DR Pfam: PF00019; TGF β -beta; 1.
 DR Pfam: PF00688; TGF β -propeptide; 1.
 DR Prodom: PD000357; TGF β ; 1.
 DR SMART: SM00204; TGF β ; 1.
 DR PROSITE: PS00250; TGF β _BETA_1; 1.
 KW Glycoprotein.
 FT NON_TER 1 185
 SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;
 Query Match 93.3%; Score 588; DB 6; Length 185;
 Best Local Similarity 94.4%; Pred. No. 1e-60;
 Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 60
 DB 79 DFGLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 138
 QY 61 VHQANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 107
 DB 133 VHQANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 185
 RESULT 12
 Q90YX0 PRELIMINARY; PRT; 389 AA.
 AC Q90YX0;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Myostatin.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kocaba A.M., Liu Z.J.;
 RT Molecular characterization and expression of the myostatin gene from
 channel catfish (Ictalurus punctatus).
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC EMBL: AF396747; AAK84666.1; -
 DR EMBL: AF396747; AAK84666.1; -
 DR InterPro: IPR001839; TGF β .
 DR InterPro: IPR001111; TGF β .N.
 DR Pfam: PF00019; TGF β -beta; 1.
 DR Pfam: PF00688; TGF β -propeptide; 1.
 DR Prodom: PD000357; TGF β ; 1.
 DR PROSITE: PS00250; TGF β _BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SEQUENCE 389 AA; 43600 MW; 569FB952B79E9173 CRC64;
 Query Match 88.7%; Score 559; DB 13; Length 389;
 Best Local Similarity 88.8%; Pred. No. 5.2e-57;
 Matches 95; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 62
 DB 283 GLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 342
 QY 63 QANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 109
 DB 343 KANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 389
 RESULT 13
 Q90W05 PRELIMINARY; PRT; 385 AA.
 AC Q90W05;

DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Myostatin.
 OS Sparus aurata (gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 OX NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maccatrozzo L., Bargelloni G., Mascarello F.,
 RA Patarnello T.;
 RT Characterization of the myostatin gene in the gilthead seabream,
 RT Sparus aurata: sequence, genomic structure, and expression pattern.
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC EMBL: AF258446; AAK53544.1; -
 DR EMBL: AF258446; AAK53544.1; -
 DR InterPro: IPR001839; TGF β .
 DR InterPro: IPR001111; TGF β .N.
 DR Pfam: PF00019; TGF β -beta; 1.
 DR Pfam: PF00688; TGF β -propeptide; 1.
 DR Prodom: PD000357; TGF β ; 1.
 DR PROSITE: PS00250; TGF β _BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;
 Query Match 88.3%; Score 556; DB 13; Length 385;
 Best Local Similarity 88.1%; Pred. No. 1.e-56;
 Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 60
 DB 277 DFGLDCEHSTESRCRRPLTVDFEAFGMDWITAPKRYKANKYSGSCFEPVLOKYPHTHL 336
 QY 61 VHQANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 109
 DB 337 VHQANPBGSAAPCCTPTKMSPINMLYFNKGQIITYGKIIPAMVYDRCG 385
 RESULT 14
 Q9DD18 PRELIMINARY; PRT; 373 AA.
 AC Q9DD18;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Myostatin precursor.
 GN GDF-8.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Proactinopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Andersen O.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ostbye T.K., Gallway T.F., Nielsen C., Gabestad I., Bardal T.,
 RA Andersen O.;
 RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
 RT expressed in a variety of tissues."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

Job time : 25 secs

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AJ297267; CAC19541.2; -.
 DR EMBL: AJ316006; CAC59700.1; -.
 DR HSSP: P12643; 3BMP.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR SMART: SM00204; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Glycoprotein; Signal; 1.
 KW SIGNAL
 FT CHAIN 1 22 POTENTIAL.
 FT CHAIN 265 373 MYOSTATIN.
 SQ SEQUENCE 373 AA; 41896 MW; C641D71D83E6C4D CRC64;

Query Match 87.8%; Score 553; DB 13; Length 373;
 Best Local Similarity 87.2%; Pred. No. 2.5e-56;
 Matches 95; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Oy 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPTHL 60
 Db 265 DSGIDCDHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPTHL 324
 Oy 61 VHOANPRGASGPCCTPTKMSPINMLYFNNGSGLIYGIKIPAMVVDRCGCS 109
 Db 325 VNKANPRGTAGPCTPTKMSPINMLYFNNGSGLIYGIKIPAMVVDRCGCS 373

RESULT 15

ID 090ZD2 PRELIMINARY; PRT; 373 AA.
 AC 090ZD2;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Myostatin 1.
 CS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rescan P.-Y., Jutel I., Ralliere C.;
 RT "Two myostatin genes are differentially expressed in myotomal muscle
 of the trout (Oncorhynchus mykiss).";
 RL J. Exp. Biol. 0:0-0(2001).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL: AF273035; AK071207.1; -.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGF-beta; 1.
 DR Pfam: PF00688; TGFb_propeptide; 1.
 DR ProDom: PD000357; TGFb; 1.
 DR PROSITE: PS00250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SQ SEQUENCE 373 AA; 42049 MW; .9DD4771B5CF671EA CRC64;

Query Match 87.8%; Score 553; DB 13; Length 373;
 Best Local Similarity 87.2%; Pred. No. 2.5e-56;
 Matches 95; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Oy 1 DFGIDCDHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPTHL 60
 Db 265 DSGIDCDHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCECFVFLQKYPTHL 324
 Oy 61 VHOANPRGASGPCCTPTKMSPINMLYFNNGSGLIYGIKIPAMVVDRCGCS 109
 Db 325 VNKANPRGTAGPCTPTKMSPINMLYFNNGSGLIYGIKIPAMVVDRCGCS 373

Search completed: January 31, 2003, 18:21:08

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 8.5 Seconds
(without alignments)
531.873 Million cell updates/sec

Title: US-09-620-586b-12

Perfect score: 630
Sequence: 1 DFGLDDEHSTESRCRRYPL.....EGQIIYKRIPIAMVYDRGCGS 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Length	ID	Description
1	630	100.0	375 1 GDF8_BOVIN	018836 bos taurus
2	618	98.1	375 1 GDF8_CHICK	042220 gallus gall
3	618	98.1	375 1 GDF8_HUMAN	014793 homo sapien
4	618	98.1	375 1 GDF8_MEIQA	042221 meleagris g
5	618	98.1	375 1 GDF8_PIG	018831 sus scrofa
6	618	98.1	376 1 GDF8_MOUSE	008689 mus musculu
7	618	98.1	376 1 GDF8_RAT	035312 rattus norv
8	612	97.1	375 1 GDF8_PAPHA	018828 papio hamad
9	608	96.5	375 1 GDF8_SHEEP	018830 ovis aries
10	573	91.0	405 1 GDF8_MOUSE	092104 mus musculu
11	573	91.0	407 1 GDF8_HUMAN	095390 homo sapien
12	559	88.7	374 1 GDF8_BRARE	042222 brachydanto
13	526	83.5	345 1 GDF8_RAT	092217 rattus norv
14	525	39.8	355 1 IHBB_MOUSE	004999 mus musculu
15	246	39.0	391 1 IHBB_CHICK	P27093 gallus gall
16	245	38.9	349 1 IHBB_PIG	P04088 sus scrofa
17	245	38.9	407 1 IHBB_HUMAN	P09529 homo sapien
18	245	38.9	408 1 IHBB_BOVIN	P42917 bos taurus
19	243	38.6	355 1 DVRI_BRARE	P35621 brachydanto
20	232.5	36.9	207 1 BMP6_RAT	Q04906 rattus norv
21	232.5	36.9	513 1 BMP6_HUMAN	Q02004 homo sapien
22	230.5	36.6	510 1 BMP6_MOUSE	P02722 mus musculu
23	219.5	34.8	426 1 IHBA_HORSE	P55102 equus caball
24	219	34.8	350 1 DAF7_CAEEL	P92172 caenorhabdi
25	218.5	34.7	125 1 GDF6_MOUSE	P43028 mus musculu
26	218.5	34.7	436 1 GDF6_BOVIN	P55106 bos taurus
27	216.5	34.4	352 1 IHBC_MOUSE	P55103 xenopus lae
28	216.5	34.4	360 1 DVRI_XENLA	P30886 xenopus lae
29	214.5	33.9	426 1 BMP7_XENLA	Q04998 mus musculu
30	213.5	33.9	424 1 IHBA_MOUSE	P03970 mus scrofa
31	213.5	33.9	424 1 IHBA_PIG	P18331 rattus norv
32	213.5	33.9	425 1 IHBA_RAT	P07995 bos taurus
33	213.5	33.9	425 1 IHBA_BOVIN	

34	213.5	33.9	425 1 IHBA_SHEEP	P43032 ovis aries
35	213.5	33.9	426 1 IHBA_HUMAN	P08476 homo sapien
36	212.5	33.7	350 1 IHBE_MOUSE	O08717 mus musculu
37	212.5	33.7	350 1 IHBE_RAT	O08959 rattus norv
38	212.5	33.7	402 1 BMP8_HUMAN	P34820 homo sapien
39	212.5	33.7	431 1 BMP7_HUMAN	P18075 homo sapien
40	211.5	33.6	151 1 GDF7_MOUSE	P43029 mus musculu
41	211.5	33.6	350 1 IHBE_HUMAN	P58166 homo sapien
42	211.5	33.6	352 1 IHBC_HUMAN	P55103 homo sapien
43	210.5	33.4	430 1 BMP7_MOUSE	P23359 mus musculu
44	210.5	33.4	495 1 GDF5_MOUSE	P43027 mus musculu
45	210.5	33.4	501 1 GDF5_HUMAN	P43026 homo sapien

ALIGNMENTS

RESULT 1

ID GDF8_BOVIN STANDARD; PRT; 375 AA.

AC 018836; 018829; Q95N97;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).

GN GDF8 OR MSTN OR MH.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

LN (1)

RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.

RC STRAIN=Frilesian; TISSUE=Muscle, and Embryo;

RX MEDLINE=97458167; PubMed=9314496;

RA Kambadur R., Sharma M., Smith T.P.L., Bass J.J.;

RT "Mutations in myostatin (GDF8) in double-muscling Belgian Blue and

Piedmontese cattle."

RL Genome Res. 7:910-916(1997).

LN (2)

RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.

RC STRAIN=Holstein; TISSUE=Skeletal muscle;

RA MEDLINE=98024153; PubMed=9356471;

RT McPherron A.C., Lee S.-J.;

RL "Double muscling in cattle due to mutations in the myostatin gene."

Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

LN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=2134337; PubMed=1145380;

RA Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambadur R.;

RT "Genomic organization and neonatal expression of the bovine myostatin

gene."

RL Mol. Cell. Biochem. 220:31-37(2001).

-1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.

-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

-1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES M. SEMIMEMBRANOSUS AND M. BICEPS FEMORIS; LOW LEVELS IN OTHER HINDLIMB MUSCLES.

-1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT. LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM DAY 31 UP UNTIL LATE GESTATION.

-1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTSE CATTLE BREDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASED MUSCLE MASS OF 20-25%.

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; AF019621; AAB81508.1; --
 DR EMBL; AF019620; AAB86687.1; --
 DR EMBL; AF320398; AAG48116.1; --
 DR HSSP; P18075; IBM.
 DR InterPro; IPR001839; TGF.
 DR InterPro; IPR001111; TGF-beta.
 DR Pfam; PF000019; TGF-beta.1.
 DR Pfam; PF006688; TGF-beta.2.
 DR Pfam; PF000357; TGF-beta.3.
 DR SMART; SM00204; TGF-beta.1.
 DR SMART; SM00250; TGF-beta.1.
 DR PROSITE; PS00250; TGF-beta.1.
 DR Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
 FT SIGNAL 1 18
 FT PROPEP 19 266
 FT CHAIN 267 375
 FT DISULFID 281 340
 FT DISULFID 309 372
 FT DISULFID 313 374
 FT DISULFID 339 374
 FT CARBOHYD 47 47
 FT CARBOHYD 71 71
 FT VARIANT 94 94
 FT VARIANT 313 313
 FT CONFLICT 14 14
 FT SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 C6C64;
 Query Match 100.0%; Score 630; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 5.3e-63;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIIAPRRYKANCSECEVFLOKYPHTL 60
 DB 267 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIIAPRRYKANCSECEVFLOKYPHTL 326
 QY 61 VHOANPRGSAQCCTPTKSPIMLYFNKGQIYKGIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAQCCTPTKSPIMLYFNKGQIYKGIIPAMVVDRCGCS 375

RESULT 2
 ID_GDF8_CHICK STANDARD; PRT; 375 AA.
 AC 042220;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Skeletal muscle;
 RA MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C.; Lee S.-U.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461 (1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC EMBL; AF019621; AAB86688.1; --
 DR EMBL; AF019620; AAB86687.1; --
 DR HSSP; P18075; IBM.
 DR InterPro; IPR001839; TGF.
 DR InterPro; IPR001111; TGF-beta.
 DR Pfam; PF000019; TGF-beta.1.
 DR Pfam; PF006688; TGF-beta.2.
 DR Pfam; PF000357; TGF-beta.3.
 DR SMART; SM00204; TGF-beta.1.
 DR SMART; SM00250; TGF-beta.1.
 DR PROSITE; PS00250; TGF-beta.1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 266
 FT CHAIN 267 375
 FT DISULFID 281 340
 FT DISULFID 309 372
 FT DISULFID 313 374
 FT DISULFID 339 374
 FT CARBOHYD 71 71
 FT SEQUENCE 375 AA; 42707 MW; DA732DB9426B4D4F C6C64;
 Query Match 98.1%; Score 618; DB 1; Length 375;
 Best Local Similarity 98.2%; Pred. No. 1.2e-61;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIIAPRRYKANCSECEVFLOKYPHTL 60
 DB 267 DFGDCDEHSTESRCRYPPLTVDFEAFGMDWIIAPRRYKANCSECEVFLOKYPHTL 326
 QY 61 VHOANPRGSAQCCTPTKSPIMLYFNKGQIYKGIIPAMVVDRCGCS 109
 DB 327 VHOANPRGSAQCCTPTKSPIMLYFNKGQIYKGIIPAMVVDRCGCS 375

RESULT 3
 ID_GDF8_HUMAN STANDARD; PRT; 375 AA.
 AC 014793;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA MEDLINE=99061972; PubMed=9843994;
 RA Gonzalez-Cadavid N.F.; Taylor W.E.; Yarasheski K.; Sinha-Hikim I.;
 RA Ma K.; Ezat S.; Shen R.; Lalani R.; Asa S.; Mamula M.; Nair G.;
 RA Arner S.; Bhasin S.;
 RT "Organization of the human myostatin gene and expression in healthy
 RT men and HIV-infected men with muscle wasting."
 RT Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943 (1998).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF019627; AAB86694.1; -
 CC EMBL: AF104922; AAC96327.1; -
 CC HSSP: P18075; IBMP.
 CC Genew: HGNC:4223; GDF8.
 CC MIM: 601788; -
 CC InterPro: IPR001839; TGFp.
 CC InterPro: IPR001111; TGFp N.
 CC Pfam: PF000019; TGF-beta; 1.
 CC Pfam: PF00688; TGFp_propeptide; 1.
 CC ProDom: PD000357; TGFp; 1.
 CC SMART: SM00204; TGFp; 1.
 CC PROSITE: PS00250; TGF_BETA_1; 1.
 CC Growth factor; Cytokine; Glycoprotein; Signal.
 CC Growth factor; Cytokine; Glycoprotein; Signal.
 CC SIGNAL. 23
 CC PROPEP 24 266 POTENTIAL.
 CC CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
 CC DISULFID 281 340 BY SIMILARITY.
 CC DISULFID 309 372 BY SIMILARITY.
 CC DISULFID 313 374 BY SIMILARITY.
 CC DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
 CC CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 375 AA; 42750 MW; EBF6129725BEAFA CRC64;
 CC -----
 CC Query Match 98.1%; Score 618; DB 1; Length 375;
 CC Best local similarity 98.2%; Pred. No. 1.2e-61;
 CC Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPRRYKANYCSGCECFVFLQKYPHTL 60
 CC 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPRRYKANYCSGCECFVFLQKYPHTL 326
 CC 61 VQANPRGSAQCCTPTKMSPINMLYFNKGGOIYIGKIPAMVVRGCGS 109
 CC 327 VQANPRGSAQCCTPTKMSPINMLYFNKGGOIYIGKIPAMVVRGCGS 375
 CC -----
 CC RESULT 4
 CC ID GDF8_MELGA STANDARD; PRT; 375 AA.
 CC AC 042221;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 CC GN GDF8 OR MSTN.
 CC OS Melagris gallinavo (Common turkey).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Actinoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 CC NCBI_TaxID=9103;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RX TISSUE=Skeletal muscle;
 CC RX MEDLINE=98024153; PubMed=9356471;
 CC RA McPherron A.C.; Lee S.-U.;
 CC RT "Double muscling in cattle due to mutations in the myostatin gene."
 CC RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461 (1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 CC EMBL: AF019625; AAB86692.1; ALT_INIT.
 CC HSSP: P18075; IBMP.
 CC InterPro: IPR001839; TGFp.
 CC InterPro: IPR001111; TGFp N.
 CC Pfam: PF000019; TGF-beta; 1.
 CC Pfam: PF00688; TGFp_propeptide; 1.
 CC ProDom: PD000357; TGFp; 1.
 CC SMART: SM00204; TGFp; 1.
 CC PROSITE: PS00250; TGF_BETA_1; 1.
 CC Growth factor; Cytokine; Glycoprotein; Signal.
 CC Growth factor; Cytokine; Glycoprotein; Signal.
 CC SIGNAL. 23
 CC PROPEP 24 266 POTENTIAL.
 CC CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
 CC DISULFID 281 340 BY SIMILARITY.
 CC DISULFID 309 372 BY SIMILARITY.
 CC DISULFID 313 374 BY SIMILARITY.
 CC DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
 CC CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 375 AA; 42784 MW; D2AEAB732ABE4E77 CRC64;
 CC -----
 CC Query Match 98.1%; Score 618; DB 1; Length 375;
 CC Best local similarity 98.2%; Pred. No. 1.2e-61;
 CC Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC -----
 CC 1 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPRRYKANYCSGCECFVFLQKYPHTL 60
 CC 267 DFGLDCEHSTESRCRYPPLTVDFEAFGMDWIAPRRYKANYCSGCECFVFLQKYPHTL 326
 CC 61 VQANPRGSAQCCTPTKMSPINMLYFNKGGOIYIGKIPAMVVRGCGS 109
 CC 327 VQANPRGSAQCCTPTKMSPINMLYFNKGGOIYIGKIPAMVVRGCGS 375
 CC -----
 CC RESULT 5
 CC ID GDF8_PIG STANDARD; PRT; 375 AA.
 CC AC 018831;
 CC DT 15-JUL-1999 (Rel. 38, Created)
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 CC GN GDF8 OR MSTN.
 CC OS Sus scrofa (Pig).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9623;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RX TISSUE=Skeletal muscle;
 CC RX MEDLINE=98024153; PubMed=9356471;
 CC RA McPherron A.C.; Lee S.-U.;
 CC RT "Double muscling in cattle due to mutations in the myostatin gene."
 CC RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461 (1997).
 CC [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=Duroc, Hampshire, Meishan, and Yorkshire;
 CC RC TISSUE=Skeletal muscle;
 CC RA Voelker G.R.; Conroy J.C.; Wheeler M.B.;
 CC RT "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
 CC RT Yorkshire pigs.";
 CC RT Submitted (Sep-1999) to the EMBL/Genbank/DBJ databases.
 CC [3]
 CC RP SEQUENCE OF 1-10 AND 36-375 FROM N.A.
 CC RX TISSUE=Muscle;
 CC RA Daneau I.; Silversides D.W.;
 CC RT Submitted (Sep-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.

```

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL: AF019623; AAB6690.1; -
DR EMBL: AF188635; AAF02770.1; -
DR EMBL: AF188636; AAF02771.1; -
DR EMBL: AF188637; AAF02772.1; -
DR EMBL: AF188638; AAF02773.1; -
DR EMBL: AF033855; AAC08035.1; -
DR EMBL: AF093798; AAC62489.1; -
DR HSSP: P18075; IBMF.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF000019; TGF-beta; I.
DR Pfam: PF00688; TGFb propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
KW SIGNAL.
FT PROPEP 1 23 POTENTIAL.
FT CHAIN 24 266 POTENTIAL.
FT DISULFID 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 375 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC....) (POTENTIAL).
SQ SEQUENCE 375 AA; 42791 MW; 0F658685FDM3418 CRC64;

Query Match 98.1%; Score 618; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 1.2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPRKRYKANYCGSECFVFLQKYPTHTL 60
DB 267 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPRKRYKANYCGSECFVFLQKYPTHTL 326
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 375

RESULT 6
GDP8 MOUSE STANDARD; PRT; 376 AA.
ID GDP8_MOUSE
AC 008689;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDP8 OR MSTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CD-1; TISSUE=Skeletal muscle;
RA MEDLINE=97284412; PubMed=9139826;
RA McPherron A.C.; Lawler A.M.; Lee S.-J.;
RT "Regulation of skeletal muscle mass in mice by a new TGF-beta
RT superfamily member."
RL Nature 387:83-90(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.

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CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
CC SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONITUM IN
CC ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
CC MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
CC CONTINUES IN ADULTHOOD.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: U84005; AAC53167.1; -
DR HSSP: P18075; IBMF.
DR MGD: MGI:95691; Gdf8.
DR InterPro: IPR001839; Gdf8.
DR InterPro: IPR001111; TGFb.N.
DR Pfam: PF000019; TGF-beta; I.
DR Pfam: PF00688; TGFb propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
KW SIGNAL.
FT PROPEP 1 24 POTENTIAL.
FT CHAIN 25 267 POTENTIAL.
FT DISULFID 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 282 341 BY SIMILARITY.
FT DISULFID 310 373 BY SIMILARITY.
FT DISULFID 314 375 BY SIMILARITY.
FT DISULFID 340 375 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC....) (POTENTIAL).
SQ SEQUENCE 376 AA; 42921 MW; 3E19814DD62C08BE CRC64;

Query Match 98.1%; Score 618; DB 1; Length 376;
Best Local Similarity 98.2%; Pred. No. 1.2e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPRKRYKANYCGSECFVFLQKYPTHTL 60
DB 268 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIAPRKRYKANYCGSECFVFLQKYPTHTL 327
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 109
DB 328 VHOANPRGSAGPCCPTPKMSPINMLYFNGEGQIIYGIKIPAMVVDRCGCS 376

RESULT 7
GDP8 RAT STANDARD; PRT; 376 AA.
ID GDP8_RAT
AC 035312;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDP8 OR MSTN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Skeletal muscle;
RA MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C.; Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene."
RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.

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CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL: AF019624; AAB86691.1; -.
CC HSSP: P18075; IBM.
CC InterPro: IPR001839; TGFb.
CC InterPro: IPR001111; TGFb.N.
CC Pfam: PF00019; TGF-beta; 1.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 24
CC PROPEP 25 267 POTENTIAL.
CC CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
CC DISULFID 282 341 BY SIMILARITY.
CC DISULFID 310 373 BY SIMILARITY.
CC DISULFID 314 375 BY SIMILARITY.
CC DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
CC CAROHYD 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 376 AA; 42829 MW; 93304308C8C3294B CRC64;

Query Match
Best Local Similarity 98.2%; Score 618; DB 1; Length 376;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRCPPLTVDFEAFGMDWIAPRKRYKANYSGCECFVLOKYPHTL 60
DB 268 DFGDLCDEHSTESRCRCPPLTVDFEAFGMDWIAPRKRYKANYSGCECFVLOKYPHTL 327

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
DB 328 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 376

RESULT 8
GDF8_PAPHA STANDARD; PRT; 375 AA.
ID GDF8_PAPHA
AC 018830;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [2]_TaxID=9557;
RP SEQUENCE FROM N.A.
RC TISSUE: Skeletal muscle;
RX MEDLINE=96024153; PubMed=9356471;
RA McPherron A.C.; Lee S.-J.;
RL "Double muscling in cattle due to mutations in the myostatin gene.";
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL: AF019619; AAB86686.1; -.
CC HSSP: P18075; IBM.
CC InterPro: IPR001839; TGFb.
CC InterPro: IPR001111; TGFb.N.
CC Pfam: PF00019; TGF-beta; 1.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Cytokine; Glycoprotein; Signal.
CC SIGNAL 1 23
CC PROPEP 24 266 POTENTIAL.
CC CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
CC DISULFID 281 340 BY SIMILARITY.
CC DISULFID 309 372 BY SIMILARITY.
CC DISULFID 313 374 BY SIMILARITY.
CC DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
CC CAROHYD 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 375 AA; 42688 MW; 7849B90ACAB926EA CRC64;

Query Match
Best Local Similarity 97.1%; Score 612; DB 1; Length 375;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRCPPLTVDFEAFGMDWIAPRKRYKANYSGCECFVLOKYPHTL 60
DB 267 DFGDLCDEHSTESRCRCPPLTVDFEAFGMDWIAPRKRYKANYSGCECFVLOKYPHTL 326

QY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCTPTKMSPINMLYFNGEQIITYGKIIPAMVVDRCGCS 375

RESULT 9
GDF8_SHEEP STANDARD; PRT; 375 AA.
ID GDF8_SHEEP
AC 018830;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Ovis aries (sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE: Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C.; Lee S.-J.;
RL "Double muscling in cattle due to mutations in the myostatin gene.";
CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=99318097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-T.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by
RL growth/differentiation factor 11.";
RN Nat. Genet. 22:260-264(1999).
[3]
RP SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamatsu A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the
RL BMP/FGFbeta subfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

[illegible]

DT 16-0CT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 11 precursor (bone morphogenetic protein
 GN 11)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=99171715; PubMed=10075854;
 RA Gamber L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
 RA Rosen V.,
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
 RT bud is a potent mesoderm inducer in *Xenopus* embryos.",
 RL Dev. Biol. 208:222-232(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9918097; PubMed=10391213;
 RA McPherron A.C., Lawler A.M., Lee S.-J.,
 RT "Regulation of anterior/posterior patterning of the axial skeleton by
 RT growth/differentiation factor 11.",
 RL Nat. Genet. 22:260-264(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
 CC IDENTIFY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 DR EMBL; AF100907; AAC72852.1; -
 DR EMBL; AF028333; AAF21630.1; -
 DR EMBL; AF028334; AAF21631.1; -
 DR HSSP; P18075; IBM.
 DR Genew; HGNC:4216; GDF11.
 DR MIM; 603936; -
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF000019; TGF-beta.1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 298
 FT CHAIN 29 407
 FT DOMAIN 29 407
 FT DOMAIN 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT DISULFID 371 371
 FT CARBOHYD 94 94
 SQ SEQUENCE 407 AA; 45090 MW; E8FF4E363535BA8 CRC64;
 Query Match 91.0%; Score 573; DB 1; Length 407;
 Best Local Similarity 89.0%; Pred. No. 1,3e-56;
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 299 NLGLDDEHSSRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEYFWQKYPHTL 358
 Qy 61 VHOANPRGAGPCCTPTKMSPINMLYFNGEGQIYGGIIPAMVYDRCGS 109
 Db 359 VHOANPRGAGPCCTPTKMSPINMLYFNDKQIYGGIIPAMVYDRCGS 407
 RESULT 12
 ID GDF8_BRARE STANDARD; PRT; 374 AA.
 AC 042252;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-J.,
 RT "Double muscling in cattle due to mutations in the myostatin gene.",
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 DR EMBL; AF019626; AAB86693.1; -
 DR HSSP; P18075; IBM.
 DR ZFIN; ZDB-GENE-990415-165; gdf8.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb.N.
 DR Pfam; PF000019; TGF-beta.1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 265
 FT CHAIN 266 374
 FT DISULFID 280 339
 FT DISULFID 308 371
 FT DISULFID 312 373
 FT DISULFID 338 338
 FT CARBOHYD 72 72
 FT CARBOHYD 274 274
 SQ SEQUENCE 374 AA; 42060 MW; 6302BC68562576 CRC64;
 Query Match 88.7%; Score 559; DB 1; Length 374;
 Best Local Similarity 86.2%; Pred. No. 4.5e-55;
 Matches 94; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Db 326 VNKASPRGATGACCTPTKMSPINMLYFNKGEOIYKILPSWVDRGCGS 374

RESULT 13

ID IDB_RAT STANDARD; PRT: 345 AA.

AC GDBF_RAT

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11) (Fragment).

GN GDF11 OR BMP11.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_Taxid=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Dental pulp;

RX MEDLINE=99173787; PubMed=10072786;

RA Nakashima M., Toyono T., Akamine A., Joyner A.;

RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGFBeta superfamily during mouse embryogenesis.";

RL Mech. Dev. 80:185-189(1999).

CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted (Probable).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: AF092733; AAD05266.1; -.

DR HSSP: P18075; IBMP.

DR InterPro: IPR001839; TGFb.

DR InterPro: IPR001111; TGFb_N.

DR Pfam: PF00019; TGFb-beta; 1.

DR Pfam: PF00688; TGFb propeptide; 1.

DR ProDom: PD000357; TGFb; 1.

DR SMART: SM00204; TGFb; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

DR Growth factor; Cytokine; Glycoprotein.

FT NON_TER

FT PROPEP

FT CHAIN

FT DOMAIN

FT DISUFID

FT CARBOHYD

FT NON_TER

FT SEQUENCE

Query Match

Best local similarity

Matches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DFGADCEHSTESRCGYPPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 60

Db 243 NGLGDCHEHSESRCKYPLTVDFEASGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 302

Qy 61 VHQANPRGSAGPCTPTKMSPINMLYFNKGEOIYKILPSWVDRGCGS 103

Db 303 VQANPRGSAGPCTPTKMSPINMLYFNKGEOIYKILPSWVDRGCGS 345

RESULT 14

ID IDB_MOUSE

AC 004959; 061277; STANDARD; PRT: 255 AA.

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).

GN INHB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE OF 1-234 FROM N.A.

RC STRAIN=CBA X NMRI, TISSUE=Testis;

RX MEDLINE=9534497; PubMed=7619733;

RA Ritvos O., Tuuri T., Brama M., Sainio K., Hilden K., Saxen L.,

RT Gilbert S.;

RT "Activin disrupts epithelial branching morphogenesis in developing glomerular organs of the mouse.";

RL Mech. Dev. 50:229-245(1995).

CC [2]

CC SEQUENCE OF 134-255 FROM N.A.

RX MEDLINE=93321614; PubMed=8330535;

RA Albano P.M., Groome N., Smith U.C.;

RT "Activins are expressed in preimplantation mouse embryos and in ES and EC cells and are regulated on their differentiation.";

RL Development 117:711-723(1993).

CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE, RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION, ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF ACTIVINS.

CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.

CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

CC ACTIVIN A IS A HOMODIMER OF BETA-A.

CC ACTIVIN B IS A HOMODIMER OF BETA-B.

CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

CC -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN.

CC -1- SUBCELLULAR LOCATION: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: X83376; CA58290.1; -.

DR EMBL: X69520; CA49326.1; -.

DR PIR: S31441; S31441.

DR HSSP: P12643; 3BMP.

DR MGI: 96571; Inhb.

DR InterPro: IPR001839; TGFb.

DR InterPro: IPR001111; TGFb_N.

DR Pfam: PF00019; TGFb-beta; 1.

DR Pfam: PF00688; TGFb propeptide; 1.

DR ProDom: PD000357; TGFb; 1.

DR SMART: SM00204; TGFb; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

DR Growth factor; Hormone; Glycoprotein.

FT NON_TER

FT PROPEP

FT CHAIN

FT INHIBIN

FT BETA B CHAIN.

FT DISULFID 144 152 BY SIMILARITY.
 FT DISULFID 151 220 BY SIMILARITY.
 FT DISULFID 180 252 BY SIMILARITY.
 FT DISULFID 184 254 BY SIMILARITY.
 FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
 FT CONFLICT 135 135 H -> D (IN REF. 2).
 SQ SEQUENCE 255 AA; 29178 MW; 2524B21DC64809A9 CRC64;

Query Match 39.8%; Score 251; DB 1; Length 255;
 Best Local Similarity 44.1%; Pred. No. 7, 5e-21;
 Matches 52; Conservative 16; Mismatches 36; Indels 14; Gaps 6;

Qy 3 GLDCEHSTESRCRYPLTVDFEAFGW-DWIIAPRYKANYSGCECFVFLQKYP----- 56
 Db 141 GLECDGRT--SLCCRQGFYDFRLGMDWIIAPSGYGVNCGSGCP-AYIAGVGSASS 197
 Qy 57 -HTHLVHOANPRG-SAGP---CCTPTKSPINMLYFNGEQIYIGKIPAMVVDRCGCS 109
 Db 198 FHTAVVNOYRMRLNGPYNVNSCIPFKLSWSMLYFDENIVKRDVPMIVBEGCA 255

RESULT 15
 ID THRB CHICK STANDARD; PRT: 391 AA.
 AC P27053; 073796;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inhibin beta B chain precursor (Activin beta-B chain).
 GN INHB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Rollicle;
 RA Klingner H., Halaaschek-Wiener J., Wohlrad B.K., Kuchler K., Wohlrad F.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Ovary;
 RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 311-381 FROM N.A.
 RX MEDLINE=91029482; PubMed=2225063;
 RA Mitrani E., Ziv T., Thomsen G., Shimon Y., Melton D.A., Brill A.;
 RT "Activin can induce the formation of axial structures and is expressed
 in the hypoblast of the chick.";
 RL Cell 63:495-501 (1990).
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE
 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
 INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
 FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
 GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
 ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
 EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
 SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
 ACTIVINS.
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
 INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
 INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; 271594; CA96248.1; -
 DR EMBL; AF055478; AAC14187.1; -
 DR EMBL; M61166; AAA48568.1; -
 DR EMBL; M57408; AAA03079.1; -
 DR HSSP; P18075; IBMP
 DR InterPro; IPR002400; GF_cycknot.
 DR InterPro; IPR001839; TGBD.
 DR InterPro; IPR001111; TGBD_N.
 DR Pfam; PF000019; TGF-beta; 1.
 DR Pfam; PF00688; TGBD_propeptide; 1.
 DR PRINTS; PR00438; GEGYSKNOT.
 DR ProDom; PD000357; TGBD; 1.
 DR SMART; SM00204; TGBD; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Growth factor; Hormone; Glycoprotein; Signal.
 KW SIGNAL
 FT PROPEP 1 25
 FT CHAIN 26 276
 FT DISULFID 277 391 INHIBIN BETA B CHAIN.
 FT DISULFID 280 288 BY SIMILARITY.
 FT DISULFID 287 356 BY SIMILARITY.
 FT DISULFID 316 388 BY SIMILARITY.
 FT DISULFID 320 390 BY SIMILARITY.
 FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 30 30 P -> PG (IN REF. 2).
 SQ SEQUENCE 391 AA; 43608 MW; 060017BF337AF6C CRC64;

Query Match 39.0%; Score 246; DB 1; Length 391;
 Best Local Similarity 41.5%; Pred. No. 4, 2e-20;
 Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

Qy 3 GLDCEHSTESRCRYPLTVDFEAFGW-DWIIAPRYKANYSGCECFVFLQKYP----- 56
 Db 277 GLECDGRT--NLCCRQGFYDFRLGMDWIIAPSGYGVNCGSGCP-AYIAGVGSASS 333
 Qy 57 -HTHLVHOANPRG-SAGP---CCTPTKSPINMLYFNGEQIYIGKIPAMVVDRCGCS 109
 Db 334 FHTAVVNOYRMRLNGPYNVNSCIPFKLSWSMLYFDENIVKRDVPMIVBEGCA 391

Search completed: January 31, 2003, 18:21:31
 Job time : 8.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 14 Seconds
(without alignments)
748.475 Million cell updates/sec

Title: US-09-620-586B-12

Perfect score: 630

Sequence: 1 DFGLDDEHSTESRCRCRYPL.....EGQIIYKIPAMVYDRCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73: *
1: Pirt: *
2: Pirt: *
3: Pirt: *
4: Pirt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	257	40.8	370	2	151199
2	251	39.8	255	2	148235
3	251	39.8	411	2	B41398
4	247.5	39.3	115	2	PN0506
5	245	38.9	349	1	WFGGBB
6	245	38.9	407	1	A40150
7	245	38.9	408	2	S50899
8	244.5	38.8	393	2	IS0103
9	243.5	38.5	115	2	PN0505
10	237.5	36.9	207	2	S37616
11	237.5	36.9	513	1	BHNU6
12	235.5	36.6	510	2	A57298
13	230	34.8	313	2	FN0042
14	229	34.6	350	2	TS2451
15	218.5	34.7	125	2	B54298
16	218.5	34.4	436	2	B54298
17	216.5	34.4	352	2	JCS360
18	216.5	34.4	352	2	S70580
19	216.5	34.4	360	2	A29619
20	216.5	34.4	367	2	JCS360
21	215.5	34.2	313	2	IS1284
22	215.5	34.0	426	2	JH0690
23	213.5	33.9	413	2	WFGGBB
24	213.5	33.9	424	1	WFGGBB
25	213.5	33.9	424	1	S31440
26	213.5	33.9	424	1	B40905
27	213.5	33.9	425	1	S50898
28	213.5	33.9	425	2	I47072
29	213.5	33.9	426	1	B24246

30	212.5	33.7	350	2	JCS241	activin beta E cha
31	212.5	33.7	402	2	A45056	osteogenic protein
32	212.5	33.7	431	1	BHNU7	bone morphogenetic
33	211.5	33.6	151	2	S43296	bone morphogenetic
34	211.5	33.6	352	2	JCS246	inhibin beta-C cha
35	210.5	33.4	430	2	U01184	osteogenic protein
36	210.5	33.4	495	2	S43294	bone morphogenetic
37	210.5	33.4	501	2	A54542	cartilage-derived
38	210.5	33.4	501	2	JCS247	growth/differentia
39	208	33.0	366	2	A46607	growth/differentia
40	206.5	32.8	452	2	I49542	bone morphogenetic
41	206.5	32.8	454	1	BHNU5	bone morphogenetic
42	206	32.7	366	2	A45402	transforming growth
43	203.5	32.3	461	2	S52408	SPDVR1 protein - s
44	201.5	32.0	409	2	S01825	transforming growth
45	201.5	32.0	410	2	A41397	transforming growth

ALIGNMENTS

RESULT 1
151199
activin beta B subunit - African clawed frog
C:/Species: Xenopus laevis (African clawed frog)
C:/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #ext_change 16-Jul-1999
C:/Accession: 151199
R:/Dohmann, C.E.; Hemmati-Briantou, A.; Thomsen, G.H.; Field, A.; Woolf, T.M.; Melton, Dev. Biol. 157, 474-483, 1993
A:/Title: Expression of activin mRNA during early development in Xenopus laevis.
A:/Reference number: 151199; NCID:9373083; PMID:8500654
A:/Accession: 151199
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-370 <DOH>
A:/Cross-references: GB:S61773; NID:9366027; PIDN:AAB26863.1; PID:9366028
C:/Superfamily: inhibin

Query Match 40.8%; Score 257; DB 2; Length 370;
Best local similarity 43.2%; Pred. No. 5, 8e-20;
Matches 51; Conservative 16; Mismatches 37; Indels 14; Gaps 5;

QY 3 GLDDEHSTESRCRCRYPLVYDPEARGM-DWIIAPKRYKAYCGSEPFLOKYP----- 56
DB 256 GLECDGHT--NLCCRGQFYDFELIGMNDWIIAPAGYGVNVCSSCP-AVLGVGSGASS 312
QY 57 -RTHLVHQAQPR---GSAGPCTPTKMSPTNMYFNGEQIYKIPAMVYDRCGCS 109
DB 313 PFTAVVNGYRRRGILPQTVNSCCIPFKLSTMSMLYFDEYVIVKRDVPMVIVDECGCA 370

RESULT 2
148235
inhibin beta-B chain - mouse (fragment)
N:/Alternate names: activin hb chain
C:/Species: Mus musculus (house mouse)
C:/Date: 02-Jul-1996 #sequence_revision 01-Aug-1997 #ext_change 16-Jul-1999
C:/Accession: 148235; I48266; S31441
R:/Ritvos, O.; Tucci, T.; Kramma, W.; Sainio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F. Mech. Dev. 50, 229-245, 1995
A:/Title: Activin disrupts epithelial branching morphogenesis in developing glandular org
A:/Reference number: 148235; NCID:9534497; PMID:761973
A:/Accession: 148235
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-234 <RES>
A:/Cross-references: EMBL:X83376; NID:9603571; PIDN:CAA58290.1; PID:9603572
R:/Albano, R.M.; Groome, N.; Smith, J.C. Development 117, 711-723, 1993
A:/Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A:/Reference number: 148243; NCID:93321614; PMID:8330535
A:/Accession: 148266
A:/Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA
 A.Residues: 134,'D',136-255 <ALB>
 A.Cross-references: EMBL:X69620; NID:G50147; PIDD:CAA9326.1; PIDD:G50148
 C.Superfamily: Inhibin

Query Match 39.8%; Score 251; DB 2; Length 255;
 Best Local Similarity 44.1%; Pred. No. 1.7e-19;
 Matches 52; Conservative 16; Mismatches 36; Indels 14; Gaps 6;

QY 3 GLDDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYGSGCEVFLOKYP----- 56
 DB 141 GLECDGRT--SLCCROGFIDPRLIGMDWIIAPGYGNYGSGSCP-AVLAVGPSASS 197
 QY 57 -HTLVHQAANPRG-SAGP---CCTPTKMSPIINMLYFNESGOIITGKIPAMVVDRCGS 109
 DB 198 FHTAVVQYRMKRLNPGPNVNSCCTPTKLSMSMLYFDDEYNIVKRDVPMNIVVECGCA 255

RESULT 3

Inhibin beta-B chain precursor - rat
 N.Alternate names: Inhibin/activin beta B-chain

C.Species: Rattus norvegicus (Norway rat)
 C.Date: 03-Apr-1992 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
 C.Accession: B41398; I53288; C40905
 R.Feng, Z.M.; Li, Y.P.; Chen, C.L.C.
 Mol. Endocrinol. 3, 1914-1925, 1989
 A.Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit genes
 A.Reference number: A41398; MUID:90190649; PMID:2628729

A.Accession: B41398
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-174 <PBN>
 A.Cross-references: GB:M32756; GB:M32757; NID:G204943; PIDD:AAA41438.1; PIDD:G554460
 R.Dykens, J.C.; Mayo, K.E.
 Endocrinology 135, 702-711, 1994
 A.Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin and

A.Reference number: I53288; MUID:94307180; PMID:8033818
 A.Accession: I53288
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA

A.Residues: 1-7 <RBS>
 A.Cross-references: GB:S72477; NID:G619268
 R.Esch, F.S.; Shimazaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N.
 Mol. Endocrinol. 1, 388-396, 1987
 A.Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of
 A.Reference number: A40905; MUID:90331931; PMID:2484214
 A.Accession: C40905
 A.Status: preliminary; not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 133-411 <BSC>
 C.Superfamily: Inhibin

Query Match 39.8%; Score 251; DB 2; Length 411;
 Best Local Similarity 44.1%; Pred. No. 2.8e-19;
 Matches 52; Conservative 16; Mismatches 36; Indels 14; Gaps 6;

QY 3 GLDDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYGSGCEVFLOKYP----- 56
 DB 237 GLECDGRT--SLCCROGFIDPRLIGMDWIIAPGYGNYGSGSCP-AVLAVGPSASS 353
 QY 57 -HTLVHQAANPRG-SAGP---CCTPTKMSPIINMLYFNESGOIITGKIPAMVVDRCGS 109
 DB 354 FHTAVVQYRMKRLNPGPNVNSCCTPTKLSMSMLYFDDEYNIVKRDVPMNIVVECGCA 411

RESULT 4

PN0506
 activin beta B-2 chain - goldfish (fragment)
 N.Alternate names: gact 11
 C.Species: Carassius auratus (goldfish)
 C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C.Accession: PN0506

R.Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.B.
 Biochem. Biophys. Res. Commun. 199, 711-717, 1993
 A.Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con

A.Reference number: PN0504; MUID:93290666; PMID:8512569
 A.Accession: PN0506
 A.Molecule type: DNA
 A.Residues: 1-115 <GEW>
 C.Superfamily: Inhibin

Query Match 39.3%; Score 247.5; DB 2; Length 115;
 Best Local Similarity 43.6%; Pred. No. 1.8e-19;
 Matches 51; Conservative 13; Mismatches 40; Indels 13; Gaps 5;

QY 3 GLDDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYGSGCEVFLOKYP----- 56
 DB 1 GLECD-GTNGGLCCROGFIDPRLIGMDWIIAPGYGNYGSGSCP-AVLAVGPSASS 58
 QY 57 -HTLVHQAANPRG-SAGP---CCTPTKMSPIINMLYFNESGOIITGKIPAMVVDRCGS 108
 DB 59 FHTAVVQYRMKRLNPGPNVNSCCTPTKLSMSMLYFDDEYNIVKRDVPMNIVVECGC 115

RESULT 5

WPGSBA
 Inhibin beta-B chain precursor - pig (fragment)

C.Species: Sus scrofa domestica (domestic pig)
 C.Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
 C.Accession: A01394
 R.Mason, A.J.; Haylick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.;
 Nature 318, 659-663, 1985
 A.Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
 A.Reference number: A93371; MUID:86092207; PMID:2417121

A.Accession: A01394
 A.Molecule type: mRNA
 A.Residues: 1-349 <MAS>

A.Cross-references: GB:X03267; NID:G2005; PIDD:CAA27021.1; PIDD:G2006
 C.Comment: The source of this protein is ovarian follicular fluid.
 C.Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
 C.Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
 C.Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle
 C.Superfamily: Inhibin
 C.Keywords: contraceptive; follicle; follicle; follicle; follicle; follicle; follicle; follicle
 F.1-349/Domain: propeptide (fragment) #status predicted <PRO>
 F.235-349/Product: inhibin beta-B chain (covalent) #status predicted

Query Match 38.9%; Score 245; DB 1; Length 349;
 Best Local Similarity 41.5%; Pred. No. 1.1e-16;
 Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYGSGCEVFLOKYP----- 56
 DB 235 GLECDGRT--NLCCROGFIDPRLIGMDWIIAPGYGNYGSGSCP-AVLAVGPSASS 291
 QY 57 -HTLVHQAANPRG-SAGP---CCTPTKMSPIINMLYFNESGOIITGKIPAMVVDRCGS 109
 DB 232 FHTAVVQYRMKRLNPGPNVNSCCTPTKLSMSMLYFDDEYNIVKRDVPMNIVVECGCA 349

RESULT 6

AA0150
 Inhibin beta-B chain precursor - human

N.Alternate names: activin AB chain B
 C.Species: Homo sapiens (man)
 C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000
 C.Accession: A40150; G24248; A40156; S10751
 R.Mason, A.J.; Berkemeier, L.M.; Schmeizler, C.H.; Schwall, R.H.
 Mol. Endocrinol. 3, 1352-1358, 1989
 A.Title: Activin B: precursor sequences, genomic structure and in vitro activities.
 A.Reference number: A40150; MUID:90114200; PMID:2575216
 A.Accession: A40150
 A.Molecule type: DNA
 A.Residues: 1-407 <MAS>

A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
 R:Macon, R.J.; Niall, H.D.; Seeburg, P.H.
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986
 A:Title: Structure of two human ovarian inhibins.
 A:Reference number: A90123; MUID:86186863; PMID:3754442
 A:Accession: C24248
 A:Molecule type: mRNA
 A:Residues: 55-407 <MA2>
 A:Cross-references: GB:M3437; NID:g186416; PIDN:AAA59169.1; PID:g186417
 R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
 Mol. Endocrinol. 3, 939-948, 1989
 A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
 A:Reference number: A40156; MUID:89295443; PMID:2739657
 A:Accession: A40156
 A:Molecule type: mRNA
 A:Residues: 22-46, 'A', 48-407 <FEN>
 A:Cross-references: GB:M31632
 A:Experimental source: testis
 R:Schmeizler, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Macon, A.J.; Liegeois, N.
 Biochim. Biophys. Acta 1039, 135-141, 1990
 A:Title: Purification and characterization of recombinant human activin B.
 A:Reference number: S10751; MUID:90304183; PMID:2364091
 A:Accession: S10751
 A:Molecule type: protein
 A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
 A:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
 C:Genetics:
 A:Gene: GDB:INHBB
 A:Cross-references: GDB:119347; OMIM:147390
 A:Map position: 2cen-2q13
 A:Superfamily: inhibin
 C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-297/Domain: propeptide #status predicted <PRO>
 F:297/Product: inhibin beta-B chain #status predicted <MAT>
 F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.9%; Score 245; DB 1; Length 407;
 Best Local Similarity 41.5%; Pred. No. 1.2e-18;
 Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

Qy 3 GLDCDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYSGCECFVLOKYP----- 56
 Db 293 GLECDGRT--NLCCROQFPIDFRLIGNWDWIIAPGYGNYCEGSCP-AYLAQVPSAS 349

Qy 57 -HTHLVHQANPR-----GSAGPCCTPTKSPINMLYENGQIIYKGIIPAWVDRCCGS 109
 Db 350 FHTAVVQYRMKRGISPSVNSCIPITKLSTMSMLYFDDEYNIYKRDVPMNIVECGCA 407

RESULT 7
 S50899
 betab inhibin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S50899
 R:Thompson, D.A.; Cronin, C.N.; Martin, F.
 Eur. J. Biochem. 226, 751-764, 1994
 A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A) - and beta(B) DNase I footprinting.
 A:Reference number: S50897; MUID:95112839; PMID:7813465
 A:Accession: S50899
 A:Molecule type: DNA
 A:Residues: 1-408 <THO>
 A:Cross-references: EMBL:U16240
 C:Genetics:
 A:Functions: 151/1
 C:Superfamily: inhibin

Query Match 38.9%; Score 245; DB 2; Length 408;
 Best Local Similarity 41.5%; Pred. No. 1.2e-18;

Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

Qy 3 GLDCDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYSGCECFVLOKYP----- 56
 Db 294 GLECDGRT--NLCCROQFPIDFRLIGNWDWIIAPGYGNYCEGSCP-AYLAQVPSAS 350

Qy 57 -HTHLVHQANPR-----GSAGPCCTPTKSPINMLYENGQIIYKGIIPAWVDRCCGS 109
 Db 351 FHTAVVQYRMKRGISPSVNSCIPITKLSTMSMLYFDDEYNIYKRDVPMNIVECGCA 408

RESULT 8
 I50103
 activin beta B - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: I50103
 R:Mittrich, J.; Rosa, F.M.
 Gene Dev. 8, 1448-1462, 1994
 A:Title: Disruption of mesoderm and axis formation in fish by ectopic expression of activin.
 A:Reference number: I50103; MUID:95011555; PMID:7926744
 A:Accession: I50103
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-393 <MIT>
 A:Cross-references: EMBL:X76051; NID:9516356; PIDN:CAA53636.1; PID:9516357
 C:Genetics:
 A:Gene: Zactbetab
 C:Superfamily: inhibin

Query Match 38.8%; Score 244.5; DB 2; Length 393;
 Best Local Similarity 41.5%; Pred. No. 1.4e-18;
 Matches 49; Conservative 17; Mismatches 39; Indels 13; Gaps 5;

Qy 3 GLDCDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYSGCECFVLOKYP----- 56
 Db 278 GLECDGN--GGLCCROQFPIDFRLIGNWDWIIAPGYGNYCEGSCP-AYLAQVPSAS 335

Qy 57 -HTHLVHQANPR-----GSAGPCCTPTKSPINMLYENGQIIYKGIIPAWVDRCCGS 109
 Db 336 FHTAVVQYRMKRGISPSVNSCIPITKLSTMSMLYFDDEYNIYKRDVPMNIVECGCA 393

RESULT 9
 P50505
 activin beta B-1 chain - goldfish (fragment)
 N:Alternate names: gact 2
 C:Species: Carassius auratus (goldfish)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: P50505
 R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E.
 Biochem. Biophys. Res. Commun. 193, 711-717, 1993
 A:Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural conservation between goldfish and human.
 A:Reference number: P50504; MUID:93290666; PMID:8512569
 A:Accession: P50505
 A:Molecule type: DNA
 A:Residues: 1-115 <GEW>
 C:Superfamily: inhibin

Query Match 38.5%; Score 242.5; DB 2; Length 115;
 Best Local Similarity 41.9%; Pred. No. 6.3e-19;
 Matches 49; Conservative 15; Mismatches 40; Indels 13; Gaps 5;

Qy 3 GLDCDHSTSRCCRYPLTVDFEAFGW-DWIIAPKRYKANYSGCECFVLOKYP----- 56
 Db 1 GLECD--GNGGLCCROQFPIDFRLIGNWDWIIAPGYGNYCEGSCP-AYLAQVPSAS 58

Qy 57 -HTHLVHQANPR-----GSAGPCCTPTKSPINMLYENGQIIYKGIIPAWVDRCCGS 108
 Db 59 FHTAVVQYRMKRGISPSVNSCIPITKLSTMSMLYFDDEYNIYKRDVPMNIVECGCA 115

RESULT 10

S37618
vgr protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
C:Accession: S37618
R:Neumann, U.; Meyerhann, R.; Schluesener, H.J.
J.Neurosci. Res. 33, 142-147, 1992
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning
A:Reference number: S37618; MUID:93085758; PMID:1453478
A:Accession: S37618
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <SAB>
A:Cross-references: EMBL:X58830; NID:957475; PIDN:CAA1634.1; PID:957476
A>Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C:Superfamily: inhibin

Query Match 36.9%; Score 232.5; DB 2; Length 207;
Best Local Similarity 42.3%; Pred. No. 1.4e-17;
Matches 47; Conservative 13; Mismatches 44; Indels 7; Gaps 2;

QY 5 DCDENHSTESRCRYPPLVDFEAFGW-DWIIAPRKRYKANYSGEGCEFFVFLQKYPHTH---- 59
DB 96 DYNSELKTRACKKHLYVSFODLGMDWIIAPRKGYANAYCDGECSPFLNANMNAITNAIV 155
QY 60 --LYHOANPRGSAAGPCTPTKMSPIINMLYNGEGQIIYGIKIPAMVYDRGCG 108
DB 156 QTLVHLMNPBYVPKCCAPTKLNAISVLYFDNSNVILKRYKNNMVAACGC 206

RESULT 11

BMH6

bone morphogenetic protein 6 precursor - human

C:Species: Homo sapiens (man)
C:Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B39263
R:Celestini, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.W.; Rosen, V.; Wang, E.A.; Wozni
Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A:Title: Identification of transforming growth factor beta family members present in bon
A:Reference number: A39263; MUID:91088608; PMID:2263636
A:Accession: B39263
A:Molecule type: mRNA
A:Residues: 1-513 <CEU>
A:Cross-references: GB:M60315; GB:M38694; NID:9339561; PIDN:AAA36737.1; PID:9339562
C:Genetics:
A:Gene: GDB:BMP6
A:Cross-references: GDB:127596; OMIM:112266
A:Map position: 6pter-6qter
C:Superfamily: inhibin
C:Keywords: bone; glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-374/Domain: propeptide #status predicted <PRO>
F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F:241,269,386,404,454/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 36.9%; Score 232.5; DB 1; Length 513;
Best Local Similarity 42.3%; Pred. No. 3.5e-17;
Matches 47; Conservative 13; Mismatches 44; Indels 7; Gaps 2;

QY 5 DCDENHSTESRCRYPPLVDFEAFGW-DWIIAPRKRYKANYSGEGCEFFVFLQKYPHTH---- 59
DB 402 DYNSELKTRACKKHLYVSFODLGMDWIIAPRKGYANAYCDGECSPFLNANMNAITNAIV 461
QY 60 --LYHOANPRGSAAGPCTPTKMSPIINMLYNGEGQIIYGIKIPAMVYDRGCG 108
DB 462 QTLVHLMNPBYVPKCCAPTKLNAISVLYFDNSNVILKRYKNNMVAACGC 512

RESULT 12

A54798

Vg-1-related protein precursor - mouse

C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A54798; A33925; S47442
R:Gitelman, S.E.; Kohrin, M.S.; Ye, J.O.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994
A:Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone
A:Reference number: A54798; MUID:94375533; PMID:8089189
A:Accession: A54798
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-510 <G17>
A:Cross-references: EMBL:X60992; NID:9530729; PIDN:CAA56917.1; PID:9530730
R:Lyons, K.; Graycar, J.L.; Lee, A.; Haslam, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, B.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A:Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transformin
A:Reference number: A33925; MUID:89282810; PMID:2734307
A:Accession: A33925
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'M', '74', 'K', '76-85', 'P', '87-510 <LYO>
A:Cross-references: GB:U04566; NID:9202352; PIDN:AAA40548.1; PID:9202353
C:Superfamily: inhibin

Query Match 36.6%; Score 230.5; DB 2; Length 510;
Best Local Similarity 42.3%; Pred. No. 5.6e-17;
Matches 47; Conservative 13; Mismatches 44; Indels 7; Gaps 2;

QY 5 DCDENHSTESRCRYPPLVDFEAFGW-DWIIAPRKRYKANYSGEGCEFFVFLQKYPHTH---- 59
DB 399 DYNSELKTRACKKHLYVSFODLGMDWIIAPRKGYANAYCDGECSPFLNANMNAITNAIV 458
QY 60 --LYHOANPRGSAAGPCTPTKMSPIINMLYNGEGQIIYGIKIPAMVYDRGCG 108
DB 459 QTLVHLMNPBYVPKCCAPTKLNAISVLYFDNSNVILKRYKNNMVAACGC 509

RESULT 13

PM0042

activin - fruit fly (Drosophila sp.) (fragment)

C:Species: Drosophila sp.
C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000
C:Accession: PM0042
R:Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.
Biochem. Biophys. Res. Commun. 246, 644-649, 1998
A:Title: Identification of a new member of transforming growth factor-beta superfamily
A:Reference number: PM0042; MUID:98289585; PMID:9618266
A:Accession: PM0042
A:Molecule type: mRNA
A:Residues: 1-373 <KUT>
A:Cross-references: GB:AF054822
C:Genetics:
A:Cross-references: FlyBase:FBgn0024913
A:Start codon: GGT
A:Initiators: 86/3
C:Superfamily: inhibin

Query Match 34.9%; Score 220; DB 2; Length 373;
Best Local Similarity 39.5%; Pred. No. 5.5e-16;
Matches 45; Conservative 17; Mismatches 40; Indels 12; Gaps 6;

QY 4 LDCDENHSTESRCRYPPLVDFEAFGW-DWIIAPRKRYKANYSGEGCEFFVFLQKYPHTH---- 57
DB 262 VDCG-GALNGQCKESFVYFKAIGMDWIIAPRKGYANAYCDGECSPFLNANMNAITNAIV 319
QY 58 THLVHGANPRG--SAGPCTPTKMSPIINMLYNGEGQIIYGIKIPAMVYDRGCG 108
DB 320 AHPIEYRKMGGLMGMRPCAPIKFSSMELIYGGD-GIIKRDLPKRVYVDEGCG 372

RESULT 14

T25451

transforming growth factor beta homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T25451

Query Match	34.8%;	Score 219;	DB 2;	Length 350;
Best Local Similarity	34.8%;	Pred. No. 6.6e-16;		
Matches 39;	Conservative 20;	Mismatches 43;	Indels 10;	Gaps 3;

QY 6 CDEHSTESRCRRYPLTYDFFAFGMDWIIAPKRYKANYCSSECF-----VFLQKYPHHTLV 61

Db 241 CNAEQSKGCGCYLDLIEIEFKIGMDWIIAPPRYNAYMCRGDCYNAHFNIAETGSKIM 300

QY 62 HQA----NPRGSAGPECTPTKMSPLNNLYFNGEGOIIYGKIPAMVVDRCGCS 109
| | | | : : : : : : : :
DB 301 RAAHKVSNP--EIGYCCHTEYDYIKLIYVNRDGRVSIA NVGMIAKKCGCS 350

bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N.Alternate names: growth and differentiation factor 6
C.Species: Mus musculus (house mouse)
C.Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C.Accession: S43295
R.Storm: E.E.; Hymn, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A.Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
A.Reference number: S43294; MUID:94195427; PMID:8145850
A.Accession: S43295
A.Molecule type: DNA
A.Residues: 1-125 <SPO>
A.Cross-references: EMBL:U08338; NID:g484863; PIDN:AAA18779.1; PID:g488464
C.Genetics:
A.Gene: Gdf6
C.Superfamily: inhibin
P.15/Domain: polybasic protease recognition site #status predicted <PFR>
F.6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted <K

Query Match	34.7%;	Score 218.5;	DB 2;	Length 125;
Best Local Similarity	39.4%;	Pred. No. 2.6e-16;		
Matches 43;	Conservative 19;	Mismatches 38;	Indels 9;	Gaps 4

Qy 9 HSTES--RCCRYPLTVDFEAFGM-DWIAPKRYKANYSGECEVEFLQKY-PHTH----- 59
| : | | | : | | | | : | : | : |
Db 16 HGKSRRLCSRKPLVNFKELGWDMIIAPLEAYAHGEGVCDEPPLRSHPLEPTNHAIQT 75

```
QY      60 LVHQANPRGSAGAPCCCTPTKSPINMLYPNGEGIIYKIPAMVVDRCGC 108
        |::|::|||::||::||::||::||::||::||::||::||
Db      76 LMSNDPFGSTPSCCVPTKLTPISILYIDAGNNVVYKQYBDMVVESSGCG 124
```

Search completed: January 31, 2003, 18:18:59
Job time : 15 secs

6

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 14 Seconds

(without alignments)
748.475 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629
Sequence: 1 DFGLDDEHSTESRCRYPL.....KEQIYKIPAMVYDRGCS 109Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	254	40.4	370	I51199	activin beta B sub
2	248	39.4	255	I48235	inhibin beta-B cha
3	248	39.4	411	B41398	inhibin beta-B cha
4	244.5	38.9	115	PN0506	inhibin beta-B-2 c
5	242	38.5	349	WPFGGB	inhibin beta-B cha
6	242	38.5	407	A40150	inhibin beta-B cha
7	242	38.5	408	S50899	betab inhibin prec
8	241.5	38.4	393	IS0103	activin beta B - z
9	239.5	38.1	115	PN0505	activin beta B-1 c
10	237.5	37.0	207	S37618	vgf protein - rat
11	237.5	37.0	513	BH406	bone morphogenetic
12	237.5	36.6	510	A54798	Vg-1-related prote
13	218.5	34.7	360	A29619	Vg1 embryonic grow
14	218.5	34.7	125	B54395	bone morphogenetic
15	218.5	34.7	436	B54352	cartilage-derived
16	218	34.7	373	PM0042	activin - fruit fl
17	217.5	34.6	413	JC4862	activin beta-A cha
18	217.5	34.6	424	WPFGGB	inhibin beta-A cha
19	217.5	34.6	424	I51440	inhibin beta-A cha
20	217.5	34.6	424	B40905	inhibin beta-A cha
21	217.5	34.6	425	I50898	inhibin beta-A cha
22	217.5	34.6	425	I47072	inhibin beta-A cha
23	217.5	34.6	426	B24248	inhibin beta-A cha
24	217.5	34.6	313	JC4151	inhibin beta-A cha
25	213.5	33.9	313	I51284	bone morphogenetic
26	213.5	33.9	352	JC5366	activin beta C - m
27	213.5	33.9	426	S70580	activin beta C pre
28	213.5	33.9	426	JH0690	bone morphogenetic
29	212.5	33.8	402	A45056	osteogenic protein

30	212.5	33.8	431	1	BH407	bone morphogenetic
31	211.5	33.6	151	2	S43296	bone morphogenetic
32	210.5	33.5	430	2	J01184	osteogenic protein
33	210.5	33.5	495	2	S43294	bone morphogenetic
34	210.5	33.5	501	2	A55452	cartilage-derived
35	208.5	33.5	501	2	JC2347	growth/differentia
36	208.5	33.1	352	2	JC2465	inhibin beta-C cha
37	208	33.1	350	2	T25451	transforming grow
38	208	33.1	366	2	A46607	growth/differentia
39	208	33.1	393	2	S37073	bone morphogenetic
40	208	33.1	394	2	S43355	bone morphogenetic
41	208	33.1	396	1	BH502	bone morphogenetic
42	208	33.1	398	2	JH0688	bone morphogenetic
43	208	33.1	398	2	JH0687	bone morphogenetic
44	207	32.9	353	2	I50607	bone morphogenetic
45	206.5	32.8	452	2	I49542	bone morphogenetic

ALIGNMENTS

RESULT 1

I51199
activin beta B subunit - African clawed frog

C/Spectes: Xenopus laevis (African clawed frog)

C/Date: 13-Sep-1996 #sequence #revision 13-Sep-1996 #ext_change 16-Jul-1999

C/Accession: I51199
R/Dohmann, C.E.; Hemmati-Brivanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melton, D.

Dev. Biol. 157, 474-483, 1993

A/Title: Expression of activin mRNA during early development in Xenopus laevis.

A/Reference number: I51199; PMID:93273083; PMID:8500654

A/Accession: I51199

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-370 <DOH>

A/Cross-references: GB:S61773; NID:G386027; PIDN:AA26863.1; PID:G386028

C/Superfamily: inhibin

Query Match 40.4%; Score 254; DB 2; Length 370;
Best Local Similarity 42.4%; Pred. No. 8e-20;
Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 5;

Db 256 GLECGHRT-MLCCRGQFYDFRLIGMNDWIIAPAGYGNCSGCP-ATLGAVERASAS 312

QY 57 -HTHVNQANPR---GSAGPCTPTKMSPIIMLYENKGEQIYKIPAMVYDRGCS 109

Db 313 FHTAVVNOYRMRGMLPGTVNSCCIPTKLSMTGMYFDDEVYIVRDPVMIVDECGCA 370

RESULT 2

I48235
inhibin beta-B chain - mouse (fragment)

N/Alternate names: activin hb chain

C/Spectes: Mus musculus (house mouse)

C/Date: 02-Jul-1996 #sequence #revision 01-Aug-1997 #ext_change 16-Jul-1999

C/Accession: I48235; I48266; S31441

R/Ritvo, O.; Tuuri, T.; Ertema, M.; Sainio, K.; Hildén, K.; Saxén, L.; Gilbert, S.F.
Mech. Dev. 50, 229-245, 1995

A/Title: Activin disrupts epithelial branching morphogenesis in developing glandular org

A/Reference number: I48235; PMID:95344997; PMID:7619733

A/Accession: I48235

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-234 <RES>

A/Cross-references: EMBL:X63376; NID:G603571; PIDN:CA58290.1; PID:G603572
R/Albano, R.M.; Groom, N.; Smith, J.C.
Development 117, 711-723, 1993
A/Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells
A/Reference number: I48235; PMID:9321614; PMID:8330535
A/Accession: I48266
A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 134,'D',136-255 <ALB>
 A:Cross-references: EMBL:X69620; NID:950147; PIDN:CAA49326.1; PTD:950148
 C:Superfamily: inhibin

Query Match 39.4%; Score 248; DB 2; Length 255;
 Best Local Similarity 43.2%; Pred. No. 2,5e-19;
 Matches 51; Conservative 17; Mismatches 36; Indels 14; Gaps 6;

3 GLDCDEHSTESRCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCECFVFLQKYP----- 56
 Db 141 GLECDERT--SLCCRQGFIDFRLIGMNDWIIAPGYGNYCESGCP-AVLAGVPSAS 137

57 -HTHLVHOANPRG-SAGP---CCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRCGC 109
 Db 198 FHTAVVNOYRMGRGLNPGVNSCCIPKLTSSMSMLYFDEYNIIVKRDVPMIVBEGCGA 255

RESULT 3

B41398
 Inhibin beta-B chain precursor - rat

N:Alternate names: inhibin/activin beta B-chain

C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Aug-1992 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999

C:Accession: B41398; I53288; C40905

R:Peng, Z.M.; Li, Y.P.; Chen, C.L.C.

Mol. Endocrinol. 3, 1914-1925, 1989

A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit ge

A:Reference number: A41398; PMID:90190649; PMID:2628729

A:Accession: B41398

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <EN>

A:Cross-references: GB:M32757; GB:M32757; NID:9204943; PIDN:AAA41438.1; PTD:9554460

R:Dykema, J.C.; Mayo, K.E.

Endocrinology 135, 702-711, 1994

A:Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin and

A:Reference number: I53288; PMID:94307180; PMID:8033818

A:Accession: I53288

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 <RES>

A:Cross-references: GB:S72477; NID:9619268

R:Bech, F.S.; Shimaoka, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Veno, N.

Mol. Endocrinol. 1, 388-396, 1987

A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of

A:Reference number: A40905; PMID:90331931; PMID:2484214

A:Accession: C40905

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 133-411 <BSC>

C:Superfamily: inhibin

Query Match 39.4%; Score 248; DB 2; Length 411;
 Best Local Similarity 43.2%; Pred. No. 4e-19;
 Matches 51; Conservative 17; Mismatches 36; Indels 14; Gaps 6;

3 GLDCDEHSTESRCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCECFVFLQKYP----- 56
 Db 297 GLECDERT--SLCCRQGFIDFRLIGMNDWIIAPGYGNYCESGCP-AVLAGVPSAS 353

57 -HTHLVHOANPRG-SAGP---CCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRCGC 109
 Db 354 FHTAVVNOYRMGRGLNPGVNSCCIPKLTSSMSMLYFDEYNIIVKRDVPMIVBEGCGA 411

RESULT 4

PN0506
 activin beta B-2 chain - goldfish (fragment)

N:Alternate names: gact 11

C:Species: Carassius auratus (goldfish)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0506

R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.B.
 Biochem. Biophys. Res. Commun. 193, 711-717, 1993
 A:Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
 A:Reference number: PN0504; PMID:9390666; PMID:8512569

Query Match 38.9%; Score 244.5; DB 2; Length 115;
 Best Local Similarity 42.7%; Pred. No. 2.6e-19;
 Matches 50; Conservative 14; Mismatches 40; Indels 13; Gaps 5;

3 GLDCDEHSTESRCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCECFVFLQKYP----- 56
 Db 1 GLECD-GTNGGLCCRQGFIDFRLIGMNDWIIAPGYGNYCESGCP-AVLAGVPSAS 58

57 -HTHLVHOANPRG-SAGP---CCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRCGC 108
 Db 59 FHTAVVNOYRMGRGLNPGVNSCCIPKLTSSMSMLYFDEYNIIVKRDVPMIVBEGCG 115

RESULT 5

WFGGB
 Inhibin beta-B chain precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000

C:Accession: A01394

R:Mason, A.J.; Hayflick, J.S.; Lang, N.; Bech, F.; Veno, N.; Ying, S.Y.; Guillemin, R.

Nature 318, 659-663, 1985

A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor

A:Reference number: A93371; PMID:86992207; PMID:2417221

A:Accession: A01394

A:Molecule type: mRNA

A:Residues: 1-349 <MS>

A:Cross-references: GB:X03267; NID:92005; PIDN:CAA27021.1; PTD:92006

C:Comment: The source of this protein is ovarian follicular fluid.

C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide

C:Comment: Different forms of inhibin have been isolated (A and B) that differ in the amino-terminal

C:Comment: inhibin is secreted by ovaries or testes and inhibits the secretion of follicl

C:Keywords: contraceptive; follicleotropin inhibitor; glycoprotein; gonad

F:1-234/Domain: propeptide (fragment) #status predicted <PRO>

F:235-349/Product: inhibin beta-B chain #status predicted <MAT>

F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.5%; Score 242; DB 1; Length 349;
 Best Local Similarity 40.7%; Pred. No. 1.5e-18;
 Matches 48; Conservative 18; Mismatches 38; Indels 14; Gaps 5;

3 GLDCDEHSTESRCRRYPLTVDFEAFGW-DWIIAPKRYKANYCSGCECFVFLQKYP----- 56
 Db 235 GLECDERT--NLCCRQGFIDFRLIGMNDWIIAPGYGNYCESGCP-AVLAGVPSAS 291

57 -HTHLVHOANPRG-SAGP---CCTPTKMSPIINMLYFNKGEQIIYGIKIPAMVYDRCGC 109
 Db 292 FHTAVVNOYRMGRGLNPGVNSCCIPKLTSSMSMLYFDEYNIIVKRDVPMIVBEGCGA 349

RESULT 6

A40150
 inhibin beta-B chain precursor - human

N:Alternate names: activin AB chain B

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Dec-2000

C:Accession: A40150; C24248; A40156; S10751

R:Mason, A.J.; Berkemeier, L.M.; Schmeizler, C.H.; Schwall, R.H.

Mol. Endocrinol. 3, 1352-1358, 1989

A:Title: Activin B: precursor sequences, genomic structure and in vitro activities.

A:Reference number: A40150; PMID:90114200; PMID:2575216

A:Accession: A40150

A:Molecule type: DNA

A:Residues: 1-407 <MS>

A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
 R:Mason, A.U.; Niall, H.D.; Seebury, P.H.
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986
 A:Title: Structure of two human ovarian inhibins.
 A:Reference number: A90123; MUID:86186863; PMID:33754442
 A:Accession: C24248
 A:Molecule type: mRNA
 A:Residues: 55-407 <MA2>
 A:Cross-references: GB:M31437; NID:g186416; PIDN:AAA59169.1; PID:g186417
 R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.
 Mol. Endocrinol. 3, 939-948, 1989
 A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
 A:Reference number: A40156; MUID:89295443; PMID:2739657
 A:Accession: A40156
 A:Molecule type: mRNA
 A:Residues: 22-46, 'A', 48-407 <FEN>
 A:Cross-references: GB:M31632
 A:Experimental source: testis
 R:Schmeltzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.U.; Liegeois, N.
 Biochem. Biophys. Acta 1039, 135-141, 1990
 A:Title: Purification and characterization of recombinant human activin B.
 A:Reference number: S10751; MUID:90304183; PMID:2364091
 A:Accession: S10751
 A:Molecule type: protein
 A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
 C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
 bin beta-A and beta-B, respectively.
 C:Genetics:
 A:Gene: GDB:INHBB
 A:Cross-references: GDB:119347; OMIM:147390
 A:Map position: 2cen-2q13
 C:Superfamily: inhibin
 C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-292/Domain: propeptide #status predicted <PRO>
 F:293/Product: inhibin beta-B chain #status predicted <MAT>
 F:33/binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 38.5%; Score 242; DB 1; Length 407;
 Best Local Similarity 40.7%; Pred. No. 1.8e-18;
 Matches 48; Conservative 18; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDGDHSTESRCRYPLTVDEAFGW-DWIIAPKRYANVCSECFVFLQKYP----- 56
 Db 293 GLECDGRT--NLCCRQGFIDRLIGMNDWIIAPGYIGNVCESCP-AVLAGVPSGASS 349

QY 57 -HTHLVHQANPR-----GSAGPCTPTKMSPINMLYFNKEQIIYGKIPAMVVDRCGS 109
 Db 350 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEVNIVKRDVPMNIVECGCA 407

RESULT 7
 S50899
 betab inhibin precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S50899
 A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A) - and beta(B) DNAse 1 footprinting.
 A:Reference number: S50897; MUID:95112839; PMID:7813465
 A:Accession: S50899
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-408 <THO>
 A:Cross-references: EMBL:U16240
 C:Genetics:
 A:introns: 151/1
 C:Superfamily: inhibin

Query Match 38.5%; Score 242; DB 2; Length 408;
 Best Local Similarity 40.7%; Pred. No. 1.8e-18;

Matches 48; Conservative 18; Mismatches 38; Indels 14; Gaps 5;

QY 3 GLDGDHSTESRCRYPLTVDEAFGW-DWIIAPKRYANVCSECFVFLQKYP----- 56
 Db 294 GLECDGRT--NLCCRQGFIDRLIGMNDWIIAPGYIGNVCESCP-AVLAGVPSGASS 350

QY 57 -HTHLVHQANPR-----GSAGPCTPTKMSPINMLYFNKEQIIYGKIPAMVVDRCGS 109
 Db 351 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEVNIVKRDVPMNIVECGCA 408

RESULT 8
 150103
 activin beta B - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: 150103
 R:Wiltbrodt, J.; Rosa, F.M.
 Genes Dev. 8, 1448-1462, 1994
 A:Title: Disruption of mesoderm and axis formation in fish by ectopic expression of activin
 A:Reference number: 150103; MUID:95011555; PMID:7926744
 A:Accession: 150103
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-393 <WIT>
 A:Cross-references: EMBL:X76051; NID:g516356; PIDN:CAA53636.1; PID:g516357
 C:Genetics:
 A:Gene: Zactbetab
 C:Superfamily: inhibin

Query Match 38.4%; Score 241.5; DB 2; Length 393;
 Best Local Similarity 40.7%; Pred. No. 1.9e-18;
 Matches 48; Conservative 18; Mismatches 39; Indels 13; Gaps 5;

QY 3 GLDGDHSTESRCRYPLTVDEAFGW-DWIIAPKRYANVCSECFVFLQKYP----- 56
 Db 278 GLECDGNN--GLCCRQGFIDRLIGMNDWIIAPGYIGNVCESCP-AVAGVPSGASS 335

QY 57 -HTHLVHQANPR-----GSAGPCTPTKMSPINMLYFNKEQIIYGKIPAMVVDRCGS 109
 Db 336 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEVNIVKRDVPMNIVECGCA 393

RESULT 9
 PN0505
 activin beta B-1 chain - goldfish (fregment)
 N:Alternate names: gact 2
 C:Species: Carassius auratus (goldfish)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: PN0505
 R:Ge, W.; Gallin, W.J.; Strobeck, C.; Peter, R.B.
 Biochem. Biophys. Res. Commun. 193, 711-717, 1993
 A:Title: Cloning and sequencing of goldfish activin subunit genes: Strong structural con
 A:Reference number: PN0504; MUID:93290666; PMID:8512569
 A:Accession: PN0505
 A:Molecule type: DNA
 A:Residues: 1-115 <GEW>
 C:Superfamily: inhibin

Query Match 38.1%; Score 239.5; DB 2; Length 115;
 Best Local Similarity 41.0%; Pred. No. 9.1e-19;
 Matches 48; Conservative 16; Mismatches 40; Indels 13; Gaps 5;

QY 3 GLDGDHSTESRCRYPLTVDEAFGW-DWIIAPKRYANVCSECFVFLQKYP----- 56
 Db 1 GLECD--GTNGGLCCRQGFIDRLIGMNDWIIAPGYIGNVCESCP-AVAGVPSGASS 58

QY 57 -HTHLVHQANPR-----GSAGPCTPTKMSPINMLYFNKEQIIYGKIPAMVVDRCGC 108
 Db 59 FHTAVVNVQYRMKGLNPGTVNSCCIPTKLSTMSMLYFDDEVNIVKRDVPMNIVECGC 115

RESULT 10

A>Title: Lfmb alterations in brachypodium mice due to mutations in a new member of the T

A:Reference number: S43294; MUID:94195427; PMID:8145850

A:Accession: S43295

A:Molecule type: DNA

A:Residues: 1-125 <STO>

A:Cross-references: EMBL:U08338; NID:9488463; PIDN:AAAI8779.1; PID:9488464

A:Gene: Gdf6

C:Superfamily: Inhibin

F:1-5/Domain: polybasic protease recognition site #status predicted <PPR>

F:6-125/Product: bone morphogenic protein homolog GDF6 (fragment) #status predicted <N

Query Match 34.7%; Score 218.5; DB 2; Length 125;

Best Local Similarity 39.4%; Pred. No. 1.9e-16;

Matches 43; Conservative 19; Mismatches 38; Indels 9; Gaps 4;

QY 9 HSTES--RCRRYPLTVDFEAFGM-DWIIAPRYKANYSGECEVFLOKY-PHTH-----59

DB 16 HGKKSRLRCRKRPLHVFKEIGMDWIIAPLEYAVHCEGCDPFIKSHLEPTNHALIQT 75

QY 60 LVHQANPRGAGAPCTPTGASPINMLYFNKKEQIIYGIKIPAMVVDRCGC 108

DB 76 LNNSMIDGSTPSCCVPTLTPLISILYIDAGNNVYKQYEDMVVESCGC 124

RESULT 15

B55452

cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000

C:Accession: B55452

R:Chang, S.C.; Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; Kozak

J. Biol. Chem. 269, 28227-28234, 1994

A>Title: Cartilage-derived morphogenetic proteins. New members of the transforming growth

A:Reference number: A55452; MUID:95050604; PMID:7961761

A:Accession: B55452

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-436 <CHA>

A:Cross-references: GB:U13661; NID:9632489; PIDN:AAA61416.1; PID:9632490

C:Superfamily: Inhibin

Query Match 34.7%; Score 218.5; DB 2; Length 436;

Best Local Similarity 38.5%; Pred. No. 6.6e-16;

Matches 42; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 9 HSTES--RCRRYPLTVDFEAFGM-DWIIAPRYKANYSGECEVFLOKY-PHTH-----59

DB 327 HGKKSRLRCRKRPLHVFKEIGMDWIIAPLEYAVHCEGCDPFIKSHLEPTNHALIQT 386

QY 60 LVHQANPRGAGAPCTPTGASPINMLYFNKKEQIIYGIKIPAMVVDRCGC 108

DB 387 LNNSMIDGSTPSCCVPTLTPLISILYIDAGNNVYKQYEDMVVESCGC 435

Search completed: January 31, 2003, 18:18:58
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 8.5 Seconds
(without alignments)

531.873 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629
Sequence: 1 DFGLDCEHSTESRCRYPL.....KEQIYGIKIPAMVDRCCGS 109

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	100.0	375	1	GDP8_CHICK
2	629	100.0	375	1	GDP8_HUMAN
3	629	100.0	375	1	GDP8_MELGA
4	629	100.0	375	1	GDP8_PIG
5	629	100.0	375	1	GDP8_MOUSE
6	629	100.0	375	1	GDP8_RAT
7	629	100.0	375	1	GDP8_PAPHA
8	619	98.4	375	1	GDP8_SHEEP
9	618	98.3	375	1	GDP8_BOVIN
10	581	92.4	405	1	GDP8_MOUSE
11	581	92.4	405	1	GDP8_HUMAN
12	570	90.6	374	1	GDP8_BRARE
13	534	84.9	345	1	GDP8_RAT
14	248	39.4	255	1	IHBB_MOUSE
15	246	39.1	355	1	DVRI_BRARE
16	243	38.6	391	1	IHBB_CHICK
17	242	38.5	349	1	IHBB_PIG
18	242	38.5	407	1	IHBB_HUMAN
19	242	38.5	408	1	IHBB_BOVIN
20	232.5	37.0	207	1	BMP6_RAT
21	232.5	37.0	513	1	BMP6_HUMAN
22	230.5	36.6	510	1	BMP6_MOUSE
23	223.5	35.5	426	1	IHBA_HORSE
24	219.5	34.9	360	1	DVRI_XENLA
25	218.5	34.7	125	1	GDP6_MOUSE
26	218.5	34.7	436	1	GDP6_BOVIN
27	217.5	34.6	424	1	IHBA_MOUSE
28	217.5	34.6	424	1	IHBA_PIG
29	217.5	34.6	424	1	IHBA_HUMAN
30	217.5	34.6	425	1	IHBA_BOVIN
31	217.5	34.6	425	1	IHBA_SHEEP
32	217.5	34.6	426	1	IHBA_HUMAN
33	213.5	33.9	352	1	IHBC_MOUSE

34	213.5	33.9	426	1	BMP7_XENLA
35	212.5	33.8	402	1	BMP8_HUMAN
36	212.5	33.8	431	1	BMP7_HUMAN
37	211.5	33.6	151	1	GDP7_MOUSE
38	210.5	33.5	430	1	BMP7_MOUSE
39	210.5	33.5	495	1	GDP5_MOUSE
40	210.5	33.5	501	1	GDP5_HUMAN
41	208.5	33.1	352	1	IHBC_HUMAN
42	208.5	33.1	395	1	UNIV_STRPU
43	208.5	33.1	424	1	IHBA_CHICK
44	208	33.1	350	1	DAF7_CAREL
45	208	33.1	366	1	GDP3_MOUSE

ALIGNMENTS

RESULT 1	ID	GDP8_CHICK	STANDARD	PRT	375 AA.
AC	042220				
DT	15-0UL-1999 (Rel. 38, Created)				
DT	15-0UL-1999 (Rel. 38, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).				
GN	GDF8 OR MSTN.				
OS	Gallus gallus (Chicken).				
OC	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=White leghorn; TISSUE=Skeletal muscle;				
RA	MEDLINE=98024153; Pubmed=9356471;				
RT	McPerron A.C., Lee S.-U.;				
RT	"Double muscling in cattle due to mutations in the myostatin gene.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).				
CC	- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL				
CC	MUSCLE GROWTH.				
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).				
CC	- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
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CC	-----				
DR	EMBL; AF019621; AAB86688.1; -				
DR	HSSP; P18075; IEMP.				
DR	InterPro; IPR001839; TGPB.				
DR	InterPro; IPR001111; TGPB.N.				
DR	Pfam; PF00019; TGF-beta.1.				
DR	Pfam; PF00068; TGF-beta.1.				
DR	Pfam; PF000357; TGF-beta.1.				
DR	SMART; SMD0204; TGF-beta.1.				
DR	SMART; SMD0250; TGF-beta.1.				
DR	Growth factor; Cytokine; Glycoprotein; Signal.				
KW	SIGNAL				
FT	PROPEP				
FT	CHAIN				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				
FT	DISULFID				
FT	CARBOHYD				
SO	SEQUENCE				
Query Match	100.0%; Score 629; DB 1; Length 375;				
Best Local Similarity	100.0%; Pred. No. 1.2e-62;				

QY 1 DFLDGDHSTESRCRPLTVDFEAFGMDWITAPRYKANYCSGCEFPVLOKYPHTL 60
 DB 267 DFLDGDHSTESRCRPLTVDFEAFGMDWITAPRYKANYCSGCEFPVLOKYPHTL 326
 QY 61 VHQANPRGAGPCCTPTKMSPINMLYNGKEQIYKIPAMVDRGCS 109
 DB 327 VHQANPRGAGPCCTPTKMSPINMLYNGKEQIYKIPAMVDRGCS 375

RESULT 4
 ID GDF8_PIG STANDARD; PRT; 375 AA.
 AC 018631;
 DT 15-JUL-1999 (Rel. 38, Last Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Duroc, Hampshire, Meishan, and Yorkshire;
 RC TISSUE=skeletal muscle;
 RA Voelker G.R., Conroy J.C., Wheeler M.B.;
 RT "Porcine myostatin cDNA sequences: Duroc, Hampshire, Meishan and
 RT Yorkshire pigs";
 RT Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-10 AND 36-375 FROM N.A.
 RC TISSUE=Muscle;
 RA Daneau I., Silversides D.W.;
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL AF019623; AAB6690.1;
 DR EMBL AF188635; AAF02770.1;
 DR EMBL AF188636; AAF02771.1;
 DR EMBL AF188637; AAF02772.1;
 DR EMBL AF188638; AAF02773.1;
 DR EMBL AF031855; AAC08035.1;
 DR EMBL AF093798; AAC62489.1;
 DR HSSP: P18075; 1BMP.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00688; TGFb_beta.1.
 DR Pfam: PF00688; TGFb_propeptide.1.
 DR ProDom: PD000357; TGFb.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; signal.
 FT SIGNAL 1 23 POTENTIAL.

FT PROBE 24 266 POTENTIAL.
 FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
 FT DISULFID 281 340 BY SIMILARITY.
 FT DISULFID 309 372 BY SIMILARITY.
 FT DISULFID 313 374 BY SIMILARITY.
 FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 375 AA; 42791 MW; 0F58685ED3418 CRC64;

Query Match 100.0%; Score 629; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.2e-62;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFLDGDHSTESRCRPLTVDFEAFGMDWITAPRYKANYCSGCEFPVLOKYPHTL 60
 DB 267 DFLDGDHSTESRCRPLTVDFEAFGMDWITAPRYKANYCSGCEFPVLOKYPHTL 326
 QY 61 VHQANPRGAGPCCTPTKMSPINMLYNGKEQIYKIPAMVDRGCS 109
 DB 327 VHQANPRGAGPCCTPTKMSPINMLYNGKEQIYKIPAMVDRGCS 375

RESULT 5
 ID GDF8_MOUSE STANDARD; PRT; 376 AA.
 AC 008659;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=skeletal muscle;
 RX MEDLINE=97284412; PubMed=9139826;
 RA McPherron A.C., Lawler A.M., Lee S.-J.;
 RT "Regulation of skeletal muscle mass in mice by a new TGF-beta
 RT superfamily member";
 RT Nature 387:83-90(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT
 CC SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-CONITUM IN
 CC ONE-THIRD OF DEVELOPING SOMITES. AT DAY 10.5, EXPRESSED IN THE
 CC MYOTOME COMPARTMENT OF SOMITES. AT LATER STAGES OF DEVELOPMENT,
 CC DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION
 CC CONTINUES IN ADULTHOOD.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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DR EMBL U84005; AAC53167.1;
 DR HSSP: P18075; 1BMP.
 DR MGD: MGI:95691; Gdf8.
 DR InterPro: IPR001839; TGFb.
 DR InterPro: IPR001111; TGFb.N.
 DR Pfam: PF00019; TGFb_beta.1.
 DR Pfam: PF00688; TGFb_propeptide.1.
 DR ProDom: PD000357; TGFb.1.
 DR SMART: SM00204; TGFb.1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.

KW Growth factor: Cytokine; Glycoprotein; Signal.
 FT SIGNL 1 24 POTENTIAL.
 FT PROPEP 25 267 POTENTIAL.
 FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
 FT DISULFID 282 341 BY SIMILARITY.
 FT DISULFID 310 373 BY SIMILARITY.
 FT DISULFID 314 375 BY SIMILARITY.
 FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 376 AA; 42921 MW; 3E19614DB62C098E CRC64;
 Query Match 100.0%; Score 629; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.2e-62;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVLOKYPHTL 60
 DB 268 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVLOKYPHTL 327
 QY 61 VHOANPRGSAGPCTPTKSPINMLYFNGKEQIITYGKIPAMVVDRCGS 109
 DB 328 VHOANPRGSAGPCTPTKSPINMLYFNGKEQIITYGKIPAMVVDRCGS 376
 RESULT 6
 GDF8_RAT STANDARD; PRT; 376 AA.
 ID GDF8_RAT
 AC 035312;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 OS GDF8 OR MSTN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-U.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
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 CC -----
 CC EMBL; AF019624; AAB86691.1; -.
 DR HSRP; P18075; IAMP.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb-propeptide; 1.
 DR Pfam; PF00688; TGFb-propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor: Cytokine; Glycoprotein; Signal.
 FT SIGNL 1 24 POTENTIAL.
 FT PROPEP 25 267 POTENTIAL.
 FT CHAIN 268 376 GROWTH/DIFFERENTIATION FACTOR 8.
 FT DISULFID 282 341 BY SIMILARITY.
 FT DISULFID 310 373 BY SIMILARITY.
 FT DISULFID 314 375 BY SIMILARITY.

FT DISULFID 340 340 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 376 AA; 42829 MW; 933043D8C83294B CRC64;
 Query Match 100.0%; Score 629; DB 1; Length 376;
 Best Local Similarity 100.0%; Pred. No. 1.2e-62;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVLOKYPHTL 60
 DB 268 DFGDGDHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYSGEGEFVLOKYPHTL 327
 QY 61 VHOANPRGSAGPCTPTKSPINMLYFNGKEQIITYGKIPAMVVDRCGS 109
 DB 328 VHOANPRGSAGPCTPTKSPINMLYFNGKEQIITYGKIPAMVVDRCGS 376
 RESULT 7
 GDF8_PAPHA STANDARD; PRT; 375 AA.
 ID GDF8_PAPHA
 AC 018828;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 OS GDF8 OR MSTN.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherron A.C., Lee S.-U.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
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 CC -----
 CC EMBL; AF019619; AAB86686.1; -.
 DR HSRP; P18075; IAMP.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00688; TGFb-propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor: Cytokine; Glycoprotein; Signal.
 FT SIGNL 1 23 POTENTIAL.
 FT PROPEP 24 266 POTENTIAL.
 FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
 FT DISULFID 281 340 BY SIMILARITY.
 FT DISULFID 309 372 BY SIMILARITY.
 FT DISULFID 313 374 BY SIMILARITY.
 FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 375 AA; 42688 MW; 7849B90ACAB926EA CRC64;
 Query Match 99.0%; Score 623; DB 1; Length 375;
 Best Local Similarity 99.1%; Pred. No. 5.8e-62;

Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCGEGEPFLQKYPHTL 60
 DB 267 DFGDDEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCGEGEPFLQKYPHTL 326

QY 61 VHOANRGSAGPCCPTTKMSPINMLYFNKGEOIYIGKIIPAVVDRCCGS 109
 DB 327 VHOANRGSAGPCCPTTKMSPINMLYFNKGEOIYIGKIIPAVVDRCCGS 375

RESULT 8
 ID GDF8_SHEEP STANDARD; PRT; 375 AA.
 AC 018830;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherson A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF019622; AAB86689.1; --
 DR HSSP; P18075; IAMP.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb N.
 DR Pfam; PF000019; TGF-beta; T.
 DR Pfam; PF006688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KM Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 23
 FT PROPEP 24
 FT CHAIN 266
 FT DISULFID 281
 FT DISULFID 309
 FT DISULFID 313
 FT DISULFID 339
 FT CARBOHYD 48
 FT CARBOHYD 71
 SQ SEQUENCE 375 AA; 42827 MW; 1C36F383BB11241 CRC64;

Query Match 98.4%; Score 619; DB 1; Length 375;
 Best Local Similarity 97.2%; Freq. No. 1.6e-61;
 Matches 106; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDDEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCGEGEPFLQKYPHTL 60
 DB 267 DFGDDEHSTESRCRRYPLTVDFEAFGMDWIAPKRYKANYCGEGEPFLQKYPHTL 326

QY 61 VHOANRGSAGPCCPTTKMSPINMLYFNKGEOIYIGKIIPAVVDRCCGS 109
 DB 327 VHOANRGSAGPCCPTTKMSPINMLYFNKGEOIYIGKIIPAVVDRCCGS 375

RESULT 9
 ID GDF8_BOVIN STANDARD; PRT; 375 AA.
 AC 018836; O18829; 095N97;
 DT 15-JUL-1999 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN OR MH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.
 RC STRAIN=Friesian; TISSUE=Muscle, and Embryo;
 RX MEDLINE=97458167; PubMed=9314496;
 RA Kamadur R., Sharma M., Smith T.P.L., Bass J.J.;
 RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and
 RT Piedmontese cattle."
 RT Genome Res. 7:910-916(1997).
 RL [2]
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.
 RC STRAIN=Holstein; TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPherson A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RT Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
 CC MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT
 CC SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES
 CC M. SEMIMEMBRANOSUS AND M. BICEPS FEMORIS; LOW LEVELS IN OTHER
 CC HINDLIMB MUSCLES.
 CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.
 CC LOW LEVELS ARE FOUND UP TO DAY 29 EMBRYOS. LEVELS INCREASE FROM
 CC DAY 31 UP UNTIL LATE GESTATION.
 CC -1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE
 CC PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE
 CC DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTSE
 CC CATTLE BREDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED
 CC NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASED
 CC MUSCLE MASS OF 20-25%.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF019761; AAB81508.1; --
 DR HSSP; AF019620; AAB86687.1; --
 DR EMBL; AF019620; AAB86687.1; --
 DR HSSP; P18075; IAMP.
 DR InterPro; IPR001839; TGFb.

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DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF BETA 1; 1.
KM Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.
FT SIGNAL 1 18
FT PROPEP 19 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 47 47
FT CARBOHYD 71 71
FT VARIANT 94 94
FT VARIANT 313 313
FT CONFLICT 14 14
SQ SEQUENCE 375 AA; 42551 MW; 84E1AB20650C05F6 CRC64;

Query Match 98.3%; Score 618; DB 1; Length 375;
Best Local Similarity 98.2%; Pred. No. 2, 1e-61;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEFPVLOKYPHTL 60
DB 267 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEFPVLOKYPHTL 326

QY 61 VQANPRGSAGPCTPTKNSPINMLYFNKGEOIYIGKIPAMVVRGCGS 109
DB 327 VQANPRGSAGPCTPTKNSPINMLYFNKGEOIYIGKIPAMVVRGCGS 375

RESULT 10
GDFB MOUSE STANDARD; PRT; 405 AA.
ID GDFB MOUSE STANDARD; PRT; 405 AA.
AC Q921M4; Q9QX55; Q9R221;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).
GN GDF11 OR BMP11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99177155; PubMed=10075854;
RA Garner L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in Xenopus embryos.";
RL Dev. Biol. 208:222-232(1999).
RN [2]
SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RA MEDLINE=9918097; PubMed=10391213;
RT McPherron A.C., Lawler A.M., Lee S.-I.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11.";
RL Nat. Genet. 22:260-264(1999).
RN [3]
SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the BMP/TGFbeta superfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

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CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESenchyme, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: AF100906; AAC72853.1; JOINED.
DR EMBL: AF100904; AAC72853.1; JOINED.
DR EMBL: AF100905; AAC72853.1; JOINED.
DR EMBL: AF028337; AAF21633.1; JOINED.
DR EMBL: AF028335; AAF21633.1; JOINED.
DR EMBL: AF028336; AAF21633.1; JOINED.
DR EMBL: AF092734; AAD05267.1; JOINED.
DR HSSP: P18075; 1BMP.
DR MGD: MGI:1338027; Gdf11.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb propeptide; 1.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF BETA 1; 1.
KM Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 296
FT CHAIN 297 405
FT DOMAIN 29 39
FT DISULFID 208 213
FT DISULFID 311 370
FT DISULFID 339 402
FT DISULFID 343 404
FT DISULFID 369 369
FT CARBOHYD 92 92
FT CONFLICT 75 75
FT CONFLICT 171 171
SQ SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;

Query Match 92.4%; Score 581; DB 1; Length 405;
Best Local Similarity 89.9%; Pred. No. 2, 9e-57;
Matches 98; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEFPVLOKYPHTL 60
DB 297 NFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEFPVLOKYPHTL 356

QY 61 VQANPRGSAGPCTPTKNSPINMLYFNKGEOIYIGKIPAMVVRGCGS 109
DB 357 VQANPRGSAGPCTPTKNSPINMLYFNKGEOIYIGKIPAMVVRGCGS 405

RESULT 11
GDFB HUMAN STANDARD; PRT; 407 AA.
ID GDFB HUMAN STANDARD; PRT; 407 AA.
AC Q95390; Q9UUD2; Q9UUD2;
DT 16-OCT-2001 (Rel. 40, Created)

```

16-OCT-2001 (Rel. 40, last sequence update)
 15-JUN-2002 (Rel. 41, last annotation update)
 Growth/differentiation factor 11 precursor (bone morphogenetic protein 11).
 GDF11 OR BMP11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI Taxid=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=99177155; PubMed=10075854;
 RA Gasser L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in Xenopus embryos."
 RL Dev. Biol. 208:222-232(1999).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99318097; PubMed=10391213;
 RA McPerron A.C., Lawler A.M., Lee S.-J.;
 RT "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11."
 RL Nat. Genet. 22:260-264(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 DR EMBL; AF100907; AAC72852.1; -;
 DR EMBL; AF028333; AAF21630.1; -;
 DR EMBL; AF028334; AAF21631.1; -;
 DR HSSP; P18075; IBMF.
 DR Genew; HGNC:4216; GDF11.
 DR MIM; 603936; -;
 DR InterPro: IPR001839; TGBP.
 DR InterPro: IPR001111; TGBP.N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR Prodom; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 DR Growth factor; Cytokine; Glycoprotein; signal.
 KW
 FT CHAIN 1 24
 FT PROPEP 25 298
 FT DOMAIN 29 407
 FT DISULFID 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT CARBOHYD 371 371
 FT CARBOHYD 94 94
 SQ SEQUENCE 407 AA; 45090 MW; E8PF48B36355BA8 CRC64;
 Query Match 92.4%; Score 581; DB 1; Length 407;
 Best Local Similarity 89.9%; Pred. No. 3e-57; Indels 0; Gaps 0;
 Matches 98; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

299 NLGDCDEHSESRCRYPFLVDFEAFGMDWIIAPKRYKANYSGCEPFVLOKYPHTHL 358
 61 VQANPRGSAGPCCPTPTKSPINMLYFNKKEOIIYKIKPAMVVDRCGS 109
 359 VQANPRGSAGPCCPTPTKSPINMLYFNKKEOIIYKIKPAMVVDRCGS 407
 RESULT 12
 GDF8_BRAE STANDARD; PRT; 374 AA.
 ID GDF8_BRAE
 AC 042222;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
 GN GDF8 OR MSTN.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 NCBI Taxid=7955;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98024153; PubMed=9356471;
 RA McPerron A.C., Lee S.-J.;
 RT "Double muscling in cattle due to mutations in the myostatin gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
 CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 DR EMBL; AF019626; AAB86693.1; -;
 DR HSSP; P18075; IBMF.
 DR ZFIN; ZDB-GENE-990415-165; gdf8.
 DR InterPro: IPR001839; TGBP.
 DR InterPro: IPR001111; TGBP.N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR Prodom; PD000357; TGF-beta; 1.
 DR SMART; SM00204; TGF-beta; 1.
 DR PROSITE; PS00250; TGF-beta; 1.
 DR Growth factor; Cytokine; Glycoprotein; signal.
 KW
 FT CHAIN 1 22
 FT PROPEP 23 365
 FT DISULFID 280 374
 FT DISULFID 308 371
 FT DISULFID 312 373
 FT DISULFID 338 338
 FT CARBOHYD 72 72
 FT CARBOHYD 274 274
 SQ SEQUENCE 374 AA; 42060 MW; 6302BC6C86562576 CRC64;
 Query Match 90.6%; Score 570; DB 1; Length 374;
 Best Local Similarity 88.1%; Pred. No. 4.5e-56; Indels 2; Gaps 0;
 Matches 96; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 326 VNKASPRGAGPCTPTKMSPINMLYFNKGEOIYKIPSWVDRGCS 374

```

RESULT 13
ID ID_HBB_MOUSE STANDARD; PRT; 345 AA.
AC Q04959; O61277;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
GN INHB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Dental pulp; PubMed=10072786;
RX MEDLINE=9913787;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the
RT BMP/TGFbeta superfamily during mouse embryogenesis.";
RL Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF092733; MAD05266.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF000019; TGF-beta.1.
DR Pfam; PF00688; TGFb propeptide.1.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF BETA.1.1.
DR Growth factor; Cytokine; Glycoprotein.
KW NON TER
FT PROPEP <1 242 BY SIMILARITY.
FT CHAIN 243 >345 GROWTH/DIFFERENTIATION FACTOR 11.
FT DOMAIN 154 159 POLY-GLY.
FT DISULFID 257 316 BY SIMILARITY.
FT DISULFID 315 315 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON TER 345 345
SQ SEQUENCE 345 AA; 39094 MW; 81D5B93FED6B0443 CRC64;
Query Match 84.9%; Score 534; DB 1; Length 345;
Best Local Similarity 88.3%; Pred. No. 4.2e-52;
Matches 91; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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RESULT 14
ID ID_HBB_MOUSE STANDARD; PRT; 255 AA.
AC Q04959; O61277;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).
GN INHB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN (1)
RP SEQUENCE OF 1-234 FROM N.A.
RC STRAIN=CBA X NHR1; TISSUE=Testis;
RX MEDLINE=9534997; PubMed=7619733;
RA Rivas O., Tuuri T., Eramaa M., Sainio K., Hilden K., Saxon L.,
RA Gilbert S.;
RT "Activin disrupts epithelial branching morphogenesis in developing
RT glandular organs of the mouse.";
RL Mech. Dev. 50:229-245(1995).
RN (2)
RP SEQUENCE OF 134-255 FROM N.A.
RX MEDLINE=9331614; PubMed=8330535;
RA Albano P.M., Groome N., Smith J.C.;
RT "Activins are expressed in preimplantation mouse embryos and in ES
RT and EC cells and are regulated on their differentiation.";
RL Development 117:711-723(1993).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING HORMONE SECRETION
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDENT ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A HOMODIMER OF BETA-A.
CC ACTIVIN B IS A HOMODIMER OF BETA-B.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- TISSUE SPECIFICITY: UTERUS, TESTIS, OVARY, LUNG, KIDNEY, BRAIN,
CC CT7 EMBRYONIC STEM CELLS, AND POSSIBLY IN LIVER.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
-----
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-----
DR EMBL; X83376; CAA58290.1; -.
DR EMBL; X69620; CAA49326.1; -.
DR PIR; S31441; S31441.
DR HSSP; P12643; 3BMP.
DR MGD; MGI:96571; Inhb.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb N.
DR Pfam; PF000019; TGF-beta.1.
DR Pfam; PF00688; TGFb propeptide.1.
DR ProDom; PD000357; TGFb.1.
DR SMART; SM00204; TGFb.1.
DR PROSITE; PS00250; TGF BETA.1.1.
DR Growth factor; Hormone; Glycoprotein.
KW NON TER
FT PROPEP <1 140 POTENTIAL.
FT CHAIN 141 255 INHIBIN BETA B CHAIN.

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FT DISULFID 144 152 BY SIMILARITY.
 FT DISULFID 151 220 BY SIMILARITY.
 FT DISULFID 180 252 BY SIMILARITY.
 FT DISULFID 184 254 BY SIMILARITY.
 FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
 FT CONFLICT 135 135 H -> D (IN REF. 2).
 SQ SEQUENCE 255 AA; 29178 MW; 2524821DC64BD9A9 CRC64;
 Query Match 39.4%; Score 248; DB 1; Length 255;
 Best Local Similarity 43.2%; Pred. No. 2e-20;
 Matches 51; Conservative 17; Mismatches 36; Indels 14; Gaps 6;
 QY 3 GLDCEHSTESRCRYPITVDFEAFGM-DWITAPRKRYKANYSGCEGFVFLQKYP-----LVH 62
 DB 141 GLECDORT--SICCRQOFIDFRLIGMNDWITAPRGYKANYSGCEGFVFLQKYP-----LVH 62
 QY 57 -HTHVAHNPFG-SAGP---CCPTKMSPINMLYFNKEQIYKIPANVYDRGCG 109
 DB 198 FHTAVNQYKRGKLPFGVNSCCIPKLSMSMLYFDEYNIVKRDVFNIVYEGCGA 255
 RESULT 15
 DVR1_BREAK STANDARD; PRT; 355 AA.
 ID DVR1_BREAK
 AC P35621;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DVR-1 protein precursor.
 GN VGI OR DVR1 OR DVR-1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=94009320; PubMed=8405668;
 RA Helde K.A., Grunwald D.J.;
 RT "The DVR-1 (Vgl) transcript of zebrafish is maternally supplied and
 RL distributed throughout the embryo.";
 RL Dev. Biol. 159:418-426(1993).
 CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
 CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
 CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
 CC DISTRIBUTED AMONG ALL BLASTOMERES.
 CC -1- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
 CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
 CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
 CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
 CC GASTRULA.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 CC EMBL; U00931; AAC2747.1; -;
 DR HSSP; P12643; 3BMP.
 DR ZFIN; ZDB-GENE-980526-389; dvrl.
 DR InterPro; IPR002400; GF_CysKnoc.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF000019; TGF_beta; I.
 DR Pfam; PF006881; TGF_beta; I.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00438; GFCYSKNOT.

DR Prodom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 15
 FT PROPEP 16 240
 FT CHAIN 241 355
 FT DISULFID 254 320
 FT DISULFID 283 352
 FT DISULFID 287 354
 FT DISULFID 319 319
 FT CARBOHYD 108 108
 FT CARBOHYD 179 179
 FT CARBOHYD 296 296
 SQ SEQUENCE 355 AA; 40201 MW; 0ED5B9850EBF322 CRC64;
 Query Match 39.1%; Score 246; DB 1; Length 355;
 Best Local Similarity 44.3%; Pred. No. 4.7e-20;
 Matches 47; Conservative 16; Mismatches 35; Indels 8; Gaps 3;
 QY 11 TESRCR-YPLTVDFEAFGM-DWITAPRKRYKANYSGCEGFVFLQKYPHT-----LVH 62
 DB 249 TFSNVCKPRRLTIDFKGVGMQDWITAPRGYKANYSGCEGFVFLQKYPHT-----LVH 62
 QY 63 QANPRGAGPCCTPTKMSPINMLYFNKEQIYKIPANVYDRGCG 108
 DB 309 SPDPKTPQPCVPIKLSPIMLYDNNNDVLRHYEDMVYDECGC 354

Search completed: January 31, 2003, 18:21:31
 Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 25 Seconds

(without alignments)
898.365 Million cell updates/sec

Title: US-09-620-586B-11

Sequence: 1 DFGDCDEHSTSRRCRYPL.....KEQIYKIPANVDRCGCS 109

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mmc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	629	100.0	162	6 Q9TSY2	Q9TSY2 sus scrofa
2	629	100.0	375	6 Q9GM97	Q9GM97 equus caball
3	629	100.0	375	6 Q95J86	Q95J86 macaca fasc
4	629	100.0	375	13 Q8UMD8	Q8UMD8 columba liv
5	629	100.0	375	13 Q8UMD7	Q8UMD7 columba ch
6	624	99.2	375	13 Q98SP0	Q98SP0 gallus gall
7	623	99.0	375	13 Q8UMD9	Q8UMD9 anser anser
8	621	98.7	375	13 Q8UMD0	Q8UMD0 anas platyr
9	618	98.3	375	6 Q8WNS6	Q8WNS6 bos taurus
10	606	96.3	185	6 Q95N11	Q95N11 capra hircu
11	599	95.2	185	6 Q9M218	Q9M218 ovis aries
12	570	90.6	389	13 Q90YX0	Q90YX0 ictalurus p
13	567	89.1	385	13 Q90W05	Q90W05 sparus aur
14	564	89.7	373	13 Q90ZD8	Q90ZD8 salmo salar
15	564	89.7	373	13 Q90ZD2	Q90ZD2 oncorhynch
16	564	89.7	373	13 Q90ZD1	Q90ZD1 oncorhynch

17	564	89.7	376	13 Q98TB4	Q98TB4 oreochromis
18	564	89.7	376	13 Q90WC9	Q90WC9 morone saxa
19	564	89.7	376	13 Q90WC8	Q90WC8 morone amer
20	563	89.5	373	13 Q90W17	Q90W17 salmo salar
21	562	89.3	376	13 Q90W06	Q90W06 umbrina cir
22	559	88.9	377	13 Q98TB3	Q98TB3 morone chry
23	557	88.6	373	13 Q98UB3	Q98UB3 salvelinus
24	554	88.1	96	13 Q9W759	Q9W759 cairina mos
25	543	86.3	359	13 Q80G53	Q80G53 equus caball
26	529	84.1	107	6 Q9BGS4	Q9BGS4 sus scrofa
27	394	62.6	78	6 Q9X586	Q9X586 equus caball
28	311	49.4	191	13 Q98TY4	Q98TY4 perca flav
29	302	48.0	104	13 Q90Z79	Q90Z79 ictalurus p
30	301.5	47.9	598	5 Q9X262	Q9X262 drosophila
31	301.5	47.9	598	5 Q9V4F4	Q9V4F4 drosophila
32	286	45.5	58	6 Q95MF3	Q95MF3 sus scrofa
33	259	41.2	263	13 Q80H11	Q80H11 umbrina cir
34	254	40.4	370	13 Q91350	Q91350 xenopus lae
35	242	38.5	395	13 Q9PWG6	Q9PWG6 anguilla ja
36	241.5	38.4	115	13 Q9DCE9	Q9DCE9 cyprinus ca
37	241.5	38.4	393	13 Q90Z61	Q90Z61 brachydanio
38	240.5	38.2	392	13 Q9PWR8	Q9PWR8 carassius a
39	239.5	38.1	115	13 Q9DGF1	Q9DGF1 cyprinus ca
40	239.5	38.1	115	13 Q9DGF0	Q9DGF0 cyprinus ca
41	239.5	38.1	115	13 Q9DGE6	Q9DGE6 oryzias lat
42	236.5	37.6	138	13 Q9MCT9	Q9MCT9 brachydanio
43	236.5	37.6	354	13 Q9YCV1	Q9YCV1 xenopus lae
44	230.5	36.6	349	5 Q97138	Q97138 brugia mala
45	226.5	36.0	361	5 Q96504	Q96504 branchiosto

ALIGNMENTS

RESULT 1

ID Q9TSY2 PRELIMINARY; PRT; 162 AA.

AC Q9TSY2; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

PT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Myostatin (Fragment).

GN MSTN.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sui.

OX NCBI_Taxid=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20078370; PubMed=10612246;

RA Strati A., Kopecky M.;

RT "Genomic organization, sequence and polymorphism of the porcine

myostatin (GDF8; MSTN) gene";

RL Anim. Genet. 30:468-470(1999).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AJ237920; CAB40844.1; ..

DR HSSP: P18075; 1BMP.

DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR001839; TGFb.

DR Pfam: PF00019; TGF-beta; 1.

DR Pfam: PF00688; TGFb_propeptide; 1.

DR PRINTS: PR00438; GFCYSKNOT.

DR PRODOM: PD000357; TGFb; 1.

DR SMART: SM00204; TGFb; 1.

DR PROSITE: PS00250; TGF_BETA_1; 1.

KW Glycoprotein.

FT NON TER

SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;

Query Match 100.0%; Score 629; DB 6; Length 162;

Best Local Similarity 100.0%; Pred. No. 1e-65;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 54 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 113
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 109
DB 114 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 162

RESULT 2
Q9GM97 PRELIMINARY; PRT; 375 AA.
AC Q9GM97;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=THROUGHBRED;
RA Hosoyama T., Yamouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AB033541; BAB16046.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Glycoprotein.
SQ
SEQUENCE 375 AA; 42736 MW; 6F424ECBEB4D9936 CRC64;

Query Match 100.0%; Score 629; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 109
DB 327 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 375

RESULT 3
Q95J86 PRELIMINARY; PRT; 375 AA.
ID Q95J86;
AC Q95J86;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN 1;
RP SEQUENCE FROM N.A.

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RC TISSUE=GASTROCNEMITUS;
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RT (Cynomolgus macaque) myostatin (GF8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AY05750; AAL17640.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
KW Glycoprotein.
SQ
SEQUENCE 375 AA; 42722 MW; 2149B46AC7D446E7 CRC64;

Query Match 100.0%; Score 629; DB 6; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 109
DB 327 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 375

RESULT 4
C8UMDB PRELIMINARY; PRT; 375 AA.
ID C8UMDB;
AC C8UMDB;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Myostatin.
GN MSTN.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeopteryx; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN 1;
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck Goose, Pigeon and Quail.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440863; AAL35277.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SQ
SEQUENCE 375 AA; 42739 MW; 88296F0A879476E CRC64;

Query Match 100.0%; Score 629; DB 13; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 267 DFGDCEHSTESRCRYPPLTVDFEAFGMDWIAPKRYKANYCSGCECFVFLQKYPHTL 326
QY 61 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 109
DB 327 VHQANPRGSAGPCTPTKSPINMLYFNKEQIITGKIIPAMVDRGCS 375

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RESULT 5
Q8UMD7 PRELIMINARY; PRT; 375 AA.
ID Q8UMD7
AC Q8UMD7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
GN Myostatin.
OS Mus musculus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Cuculiformes.
NCBI_TaxID=46218;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
SQ SEQUENCE 375 AA; 42721 MW; 8893B1IA42DE0725 CRC64;

Query Match 100.0%; Score 629; DB 13; Length 375;
Best Local Similarity 100.0%; Pred. No. 2, 4e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 60
DB 267 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 375

RESULT 6
Q98SP0 PRELIMINARY; PRT; 375 AA.
ID Q98SP0
AC Q98SP0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
GN Myostatin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; IBMF.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.

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DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00250; TGF BETA 1; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4D4F CRC64;

Query Match 99.1%; Score 624; DB 13; Length 375;
Best Local Similarity 99.1%; Pred. No. 9, 2e-65;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 60
DB 267 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 375

RESULT 7
Q8UMD9 PRELIMINARY; PRT; 375 AA.
ID Q8UMD9
AC Q8UMD9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
GN Myostatin.
OS Anser anser (domestic goose).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
NCBI_TaxID=8843;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
RT Duck, Goose, Pigeon and Quail."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF440864; AAL35278.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb propeptide; 1.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF HAND; UNKNOWN 1.
DR PROSITE; PS00250; TGF BETA 1; UNKNOWN 1.
SQ SEQUENCE 375 AA; 42667 MW; 57DDE45D3AA2978C CRC64;

Query Match 99.0%; Score 623; DB 13; Length 375;
Best Local Similarity 99.1%; Pred. No. 1, 2e-64;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 60
DB 267 DFGDGDHSTSRRCRPLTVDFEAFGMDWIIAPKRYKANYSGGCEFPVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTKMSPINMLYFNKGEOIYGIKIPAMVVDRCGCS 375

RESULT 8
Q8UMEO PRELIMINARY; PRT; 375 AA.
ID Q8UMEO
AC Q8UMEO;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

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DE MYOSTATIN.
 GN MSN.
 OS Aas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 CX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gu Z., Yang W., Cheng Z., Li H., Zhu D.;
 RT "Molecular Cloning and Tissue Distribution of the Myostatin Gene in
 RT Duck, Goose, Pigeon and Quail".
 RU Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF40861; AAL35275.1; -
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 375 AA; 42817 MW; 1BA7F525C23620 CRC64;

Query Match 98.7%; Score 621; DB 13; Length 375;
 Best Local Similarity 99.1%; Pred. No. 2.1e-64;
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 60
 DB 267 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 326
 QY 61 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 109
 DB 327 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 375

RESULT 9
 QMNS6 PRELIMINARY; PRT; 375 AA.
 AC QMNS6; 20. Created
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Myostatin.
 GN GDF8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shibata M., Muramoto T., Aikawa K.;
 RT "Genomic organization and sequence of the myostatin gene in bovine."
 RU Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB076403; BAB79496.1; -
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 SQ SEQUENCE 375 AA; 42524 MW; DEC27616C202F5E6 CRC64;

Query Match 98.3%; Score 618; DB 6; Length 375;
 Best Local Similarity 98.2%; Pred. No. 4.6e-64;
 Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 60
 DB 327 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 375

DB 267 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 326
 QY 61 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 109
 DB 327 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 375

RESULT 10
 QMNS11 PRELIMINARY; PRT; 185 AA.
 AC QMNS11; 19. Created
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Myostatin (fragment).
 GN MSN.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 CX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lian Z., Pan Q., Chen H., Jin H., Li N.;
 RT "Cloning of Intron 2 of the myostatin gene in goat."
 RU Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AY032689; AAK49790.1; -
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR PROSITE; PS000250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 FT NON_TER 1
 FT NON_TER 185
 SQ SEQUENCE 185 AA; 20953 MW; 03675B386E9D64D4 CRC64;

Query Match 96.3%; Score 606; DB 6; Length 185;
 Best Local Similarity 97.2%; Pred. No. 5.7e-63;
 Matches 104; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 60
 DB 79 DFGDCEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCECFVFLQKYPHTL 138
 QY 61 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 107
 DB 139 VHOANPRGSAAGCCTPTKMSPINMLYFNKGEOIIVGKIIPAMVVDRCG 185

RESULT 11
 QMNS18 PRELIMINARY; PRT; 185 AA.
 AC QMNS18; 15. Created
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Myostatin (fragment).
 GN MSN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 CX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lian Z., Jin H., Li N.;
 RT "Cloning of Intron 2 of the myostatin gene in sheep."
 RU Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF265758; AAF78069.1; -

DR HSBP; P12643; 38MP.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00018; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT TER 185
 SQ SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 95.2%; Score 599; DB 6; Length 185;
 Best Local Similarity 96.3%; Pred. No. 3.8e-62;
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDCEHSTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 60
 DB 79 DFGDCEHSTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 138

OY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 107
 DB 139 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 185

RESULT 12
 O90Y00 PRELIMINARY; PRT; 389 AA.

AC Q90Y00;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin.
 OS Ictalurus punctatus (Channel catfish).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 CC Ictaluridae; Ictalurus.
 OK NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kocabas A.M., Liu Z.J.;
 RT "Molecular characterization and expression of the myostatin gene from
 RT channel catfish (Ictalurus punctatus).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF396747; AAK8466.1; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SQ SEQUENCE 389 AA; 43600 MW; 569B952B7E9E173 CRC64;

Query Match 90.6%; Score 570; DB 13; Length 389;
 Best Local Similarity 90.7%; Pred. No. 2e-58;
 Matches 97; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

OY 3 GIDDCHESTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 62
 DB 283 GIDDCHESTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 342

OY 63 QANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 109
 DB 343 KANPRGTAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 389

RESULT 13
 O90M05 PRELIMINARY; PRT; 385 AA.
 AC Q90M05;

DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin.
 OS Sparus aurata (gilthead sea bream).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 CC Sparidae; Sparus.
 OK NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maccario L., Bargelloni L., Radaielli G., Mascarello F.,
 RA Patarnello T.;
 RT "Characterization of the myostatin gene in the gilthead seabream,
 RT Sparus aurata: sequence, genomic structure, and expression pattern";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF258448; AAK53545.1; -.
 DR EMBL; AF258447; AAK53544.1; -.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
 KW Glycoprotein.
 SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match 90.1%; Score 567; DB 13; Length 385;
 Best Local Similarity 89.9%; Pred. No. 4.4e-58;
 Matches 98; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

OY 1 DFGDCEHSTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 60
 DB 277 DFGDCEHSTSRCCRYPLTVDFEAFGMDWIAPRKRYKANYGSGCEPFYLOKYPHTL 336

OY 61 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 109
 DB 337 VHQANPRGSAGPCTPTKMSPINMLYFNGKEQIYGIKIPANVVDRCG 385

RESULT 14
 O9DD18 PRELIMINARY; PRT; 373 AA.

AC Q9DD18;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Myostatin precursor.
 GN GDF-8.
 OS Salmo salar (Atlantic salmon).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Procanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OK NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osby T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;
 RA Osby T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
 RA Andersen O.;
 RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
 RT expressed in a variety of tissues";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Andersen O.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Osby T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
 RA Andersen O.;
 RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
 RT expressed in a variety of tissues";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

Job time : 27 secs

CC	EMBL	Similarity	Accession	Gene	Protein	Signal	Potential
CC	EMBL	41297267	CAC19541.2	-	-	-	-
DR	EMBL	AJ316006	CAC59700.1	-	-	-	-
DR	HSSP	F12645	3BMP	-	-	-	-
DR	InterPro	IPR001839	TGFb	-	-	-	-
DR	InterPro	IPR001111	TGFb N	-	-	-	-
DR	Pfam	PF000019	TGF-beta; 1	-	-	-	-
DR	Pfam	PF006688	TGFb propeptide; 1	-	-	-	-
DR	ProDom	PD000357	TGFb; 1	-	-	-	-
DR	SMART	SM00204	TGFb; 1	-	-	-	-
DR	ProSite	PS00250	TGF_BETA_1; 1	-	-	-	-
KM	GlycoProtein	Signal	-	-	-	-	-
FT	SIGNAL	1	22	POTENTIAL	-	-	-
FT	CHAIN	265	373	MYOSTATIN	-	-	-
SO	SEQUENCE	373 AA	41896 MW	C641D7IDB3E66CAD	CRC64	-	-

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 32 seconds

(without alignments)
453.885 Million cell updates/sec

Title: us-09-620-586b-11

Sequence: 1 DFGDCEHSTESRCRRPL.....KEQIIYKIRPMYVDRGCS 109

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID2/gcgdata/geneeq/geneeq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneeq/geneeq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	629	100.0	109	22	AA20141
2	629	100.0	109	23	AA20141
3	629	100.0	126	15	AA20141
4	629	100.0	126	19	AA20141
5	629	100.0	126	20	AA20141
6	629	100.0	126	22	AA20141
7	629	100.0	130	22	AA20141
8	629	100.0	160	22	AA20141
9	629	100.0	226	22	AA20141
10	629	100.0	254	22	AA20141

11	629	100.0	362	22	AA20132	Turkey growth diff
12	629	100.0	374	23	AA20132	Chicken growth diff
13	629	100.0	375	15	AA20132	Human growth diff
14	629	100.0	375	19	AA20132	Human growth diff
15	629	100.0	375	19	AA20132	Human growth diff
16	629	100.0	375	19	AA20132	Human growth diff
17	629	100.0	375	19	AA20132	Human growth diff
18	629	100.0	375	20	AA20132	Human growth diff
19	629	100.0	375	20	AA20132	Human growth diff
20	629	100.0	375	20	AA20132	Human growth diff
21	629	100.0	375	20	AA20132	Human growth diff
22	629	100.0	375	20	AA20132	Human growth diff
23	629	100.0	375	20	AA20132	Human growth diff
24	629	100.0	375	20	AA20132	Human growth diff
25	629	100.0	375	20	AA20132	Human growth diff
26	629	100.0	375	20	AA20132	Human growth diff
27	629	100.0	375	20	AA20132	Human growth diff
28	629	100.0	375	20	AA20132	Human growth diff
29	629	100.0	375	20	AA20132	Human growth diff
30	629	100.0	375	20	AA20132	Human growth diff
31	629	100.0	375	20	AA20132	Human growth diff
32	629	100.0	375	21	AA20132	Human growth diff
33	629	100.0	375	21	AA20132	Human growth diff
34	629	100.0	375	21	AA20132	Human growth diff
35	629	100.0	375	21	AA20132	Human growth diff
36	629	100.0	375	21	AA20132	Human growth diff
37	629	100.0	375	21	AA20132	Human growth diff
38	629	100.0	375	21	AA20132	Human growth diff
39	629	100.0	375	21	AA20132	Human growth diff
40	629	100.0	375	21	AA20132	Human growth diff
41	629	100.0	375	21	AA20132	Human growth diff
42	629	100.0	375	21	AA20132	Human growth diff
43	629	100.0	375	21	AA20132	Human growth diff
44	629	100.0	375	21	AA20132	Human growth diff
45	629	100.0	375	21	AA20132	Human growth diff

ALIGNMENTS

RESULT 1	AA20141	standard; Protein; 109 AA.
XX	AA20141;	
XX	30-APR-2001	(first entry)
XX	Human growth differentiation factor 8 C-terminal region.	
XX	Growth differentiation factor 8; GDF-8; myostatin; down-regulation;	
XX	vacuole; muscle; meat; cachexia; cardiant; human; mutant; mutein.	
XX	Homo sapiens.	
XX	Synthetic.	
XX	MO200105820-A2.	
XX	25-JAN-2001.	
XX	20-JUL-2000; 2000MO-DK00413.	
XX	20-JUL-1999; 99DK-0001014.	
XX	26-JUL-1999; 99US-0145275.	
XX	(MEB-) M & E BIOTECH AS.	
XX	Halker T, Moutlsen S, Klysner S;	
XX	WPI; 2001-112680/12.	
XX	Increasing the muscle mass of animals used in meat production by down	
XX	regulating growth differentiation factor 8 (GDF-8) activity in the	

PT animal through induction of anti-GDF-8 antibody production -
 XX
 PS Claim 17, Page 93-94, 110pp; English.
 XX
 CC The present sequence comprises the 109 amino acid residue
 CC C-terminal region of human growth differentiation factor 8
 CC (GDF-8), i.e. residues 267-375 of the full-length protein (see
 CC AAB20131). The homodimer of this region is thought to be the
 CC biologically active form of GDF-8. It is an object of the
 CC invention to produce a recombinant therapeutic vaccine capable of
 CC effecting down-regulation of GDF-8 in order to increase the muscle
 CC growth rate of farm animals. Variants of GDF-8 (see AAB20145-53)
 CC are provided that are capable of breaking autotolerance against
 CC analogous GDF-8. These comprise the C-terminal portion of human
 CC GDF-8 in which a portion of the native sequence is replaced by a
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
 CC P2 or P30. The high number (9) of Cys residues in the C-terminal
 CC region limits the possible sites in which the T-cell epitope can be
 CC positioned without major disturbance of the native 3-dimensional
 CC structure of the protein. Nucleic acids encoding the GDF-8 variants
 CC can be used for genetic immunisation of the animals. Down-regulation
 CC of GDF-8 activity can increase muscle mass by up to at least 45% in
 CC cattle, pigs and poultry used for meat production, reducing the need
 CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 XX
 SQ Sequence 109 AA;
 Query Match 100.0%; Score 629; DB 22; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.8e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDCCDEHSTSRCCRYPLTVDFAFGMDWITIAKRYKANKSGGCEPFLQKYPHTL 60
 DB 1 DFGDCCDEHSTSRCCRYPLTVDFAFGMDWITIAKRYKANKSGGCEPFLQKYPHTL 60
 QY 61 VHOANPRGSAGPCCPTTKMSPINMLYFNKGEOIITYGKIIPAMVYDRCCGS 109
 DB 61 VHOANPRGSAGPCCPTTKMSPINMLYFNKGEOIITYGKIIPAMVYDRCCGS 109
 RESULT 2
 AAM51935
 ID AAM51935 standard; protein; 109 AA.
 XX
 AC AAM51935;
 XX
 DT 01-FEB-2002 (first entry)
 DE Human TGFbeta protein superfamily protein GDF8.
 XX
 KW Human; TGFbeta; transforming growth factor beta; mutant; antagonist;
 KW agonist; ectopic bone formation; psoriasis; muscular atrophy; scar;
 KW formation; fibrosis; cirrhosis; osteopathic; antipsoriatic;
 KW antifibrotic; hepatotropic; vulnary; GDF8.
 XX
 OS Homo sapiens.
 XX
 PN D010026713-A1.
 XX
 PD 06-DEC-2001.
 XX
 PF 30-MAY-2000; 2000DE-1026713.
 XX
 PR 30-MAY-2000; 2000DE-1026713.
 XX
 PA (SEBA/) SEBALD W.
 XX
 PI Sebald W, Nickel J;
 XX
 DR WPI; 2002; 042559/06.

XX
 PT New mutant of transforming growth factor-beta superfamily protein,
 PT useful for treating or preventing e.g. ectopic bone formation, competes
 PT for receptor binding -
 XX
 PS Disclosure; Fig 6; 54pp; German.
 XX
 CC The present invention relates to mutants of a chain of a protein which,
 CC when in the form of a homodimer, has antagonistic or partial agonistic
 CC activity, and where the mutation results in the protein binding with low
 CC affinity to its receptor. The protein is a member of the transforming
 CC growth factor beta (TGFbeta) superfamily. The mutant sequences of the
 CC invention can be used in the treatment of diseases associated with the
 CC overexpression of TGFbeta family proteins, including ectopic bone
 CC formation, psoriasis, muscular atrophy, scar formation, fibrosis and
 CC cirrhosis. The present sequence is the human GDF8 protein.
 XX
 SQ Sequence 109 AA;
 Query Match 100.0%; Score 629; DB 23; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2.8e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDCCDEHSTSRCCRYPLTVDFAFGMDWITIAKRYKANKSGGCEPFLQKYPHTL 60
 DB 1 DFGDCCDEHSTSRCCRYPLTVDFAFGMDWITIAKRYKANKSGGCEPFLQKYPHTL 60
 QY 61 VHOANPRGSAGPCCPTTKMSPINMLYFNKGEOIITYGKIIPAMVYDRCCGS 109
 DB 61 VHOANPRGSAGPCCPTTKMSPINMLYFNKGEOIITYGKIIPAMVYDRCCGS 109
 RESULT 3
 AAR63161
 ID AAR63161 standard; protein; 126 AA.
 XX
 AC AAR63161;
 XX
 DT 23-JUN-1995 (first entry)
 DE Mouse growth differentiation factor-8 partial sequence.
 XX
 KW Growth differentiation factor-8; GDF-8; cell proliferation;
 KW adipocyte; obesity; transforming growth factor-beta.
 XX
 OS Mus musculus.
 XX
 PN M09421681-A.
 XX
 PD 29-SEP-1994.
 XX
 PF 18-MAR-1994; 94MO-US03019.
 XX
 PR 19-MAR-1993; 93US-0033923.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
 XX
 PI Lee S, Mcpherron AC;
 XX
 PN WPI; 1994-316943/39.
 XX
 PD Q-PSDB; Q76380.
 XX
 PT New growth differentiation factor 8 - useful for treatment and
 PT diagnosis of cell proliferative disorders esp. of muscle.
 XX
 PS Disclosure; Page 41; 84pp; English.
 XX
 CC GDF-8 can be used to maintain cells before transplantation; to
 CC improve efficiency of cell fusion and to treat obesity or diseases
 CC related to abnormal adipocyte proliferation.
 XX
 SQ Sequence 126 AA;

PS Example 2, Fig 2a, 138pp; English.

XX This is the amino acid sequence of the C-terminal region of the GDF-8
CC precursor protein. The predicted GDF-8 sequence contains two potential
CC proteolytic processing sites.
CC Cleavage of the precursor at the second of these sites would generate
CC a mature C terminal fragment 109 amino acids in length with a predicted
CC molecular weight of 12,400.
CC GDF-8 has been shown to result in increased bone and muscle mass (such
CC as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
CC animals and forms of animal feed that can inhibit/reduce production of
CC GDF-8 are of commercial interest.
CC GDF-8 expression may also have a role in the therapy of abnormal growth
CC of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
CC antisense molecule or dominant negative polypeptide could be used with
CC foetal or adult muscle cells, bone cells or progenitor cells. These
CC agents can be administered to a patient suffering from a disorder such
CC as muscle wasting disease, neuro muscular disorder, muscle atrophy,
CC osteoporosis, bone degenerative diseases, obesity or other adipocyte
CC cell disorders, and aging for example.

SO Sequence 126 AA;

Query Match 100.0%; Score 629; DB 20; Length 126;
Best Local Similarity 100.0%; Pred. No. 3,3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
Db 18 DFGDLCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 77

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIIYKIPAMVVDRCGCS 109
Db 78 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIIYKIPAMVVDRCGCS 126

RESULT 6

AAB73182
ID AAB73182 standard; Protein: 126 AA.

AC AAB73182;

DT 11-MAY-2001 (first entry)

XX Murine GDF-8 #1.

XX Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musclogenenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.

OS Mus sp.

PN WO200112777-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000MO-US22884.

PR 19-AUG-1999; 99US-0378238.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

XX WPI; 2001-211209/21.

DR N-PSDB; AAF63547.

XX New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -

XX Example 2, Fig 2, 124pp; English.

XX The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), musclogenenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.

SO Sequence 126 AA;

Query Match 100.0%; Score 629; DB 22; Length 126;
Best Local Similarity 100.0%; Pred. No. 3,3e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
Db 18 DFGDLCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 77

QY 61 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIIYKIPAMVVDRCGCS 109
Db 78 VHOANPRGSAGPCTPTKMSPINMLYFNKGKQIIYKIPAMVVDRCGCS 126

RESULT 7

AAB73189
ID AAB73189 standard; Protein: 130 AA.

AC AAB73189;

DT 11-MAY-2001 (first entry)

XX Rat GDF-8.

XX Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musclogenenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.

OS Rattus sp.

PN WO200112777-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000MO-US22884.

PR 19-AUG-1999; 99US-0378238.

PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

XX WPI; 2001-211209/21.

DR N-PSDB; AAF63555.

XX New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -

XX Example 9; Fig 2, 124pp; English.

CC The present invention relates to growth differentiation factor-8 (GDF-8)

CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musculoskeletal diseases or in tissue repair due
 CC to trauma, obesity and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.
 CC
 SQ Sequence 130 AA;
 Query Match 100.0%; Score 629; DB 22; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
 DB 22 DFGDGDHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 81
 QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKEQIIYKGIPIAMVVDRCGCS 109
 DB 82 VHOANPRGSAGPCCPTPKMSPINMLYFNKEQIIYKGIPIAMVVDRCGCS 130
 RESULT 9
 AAB20153
 ID AAB20153 standard; Protein; 160 AA.
 AC AAB20153;
 DT 30-APR-2001 (first entry)
 DE Growth differentiation factor 8 AutoVac construct GDF-8 ext.
 KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
 KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
 KW cardant; human; mutant; muteln.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Clostridium tetani.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT 1..15
 FT /note= "identical to residues 215-230 of human
 FT Region GDF-8"
 FT 16..36
 FT /note= "tetanus toxoid P30 epitope"
 FT Region 37..51
 FT /note= "tetanus toxoid P2 epitope"
 FT Region 52..160
 FT /note= "identical to residues 267-375 of human
 FT Region GDF-8"
 FT 124
 FT /note= "Cys-124 may be substituted by Ser to avoid
 FT Misc-difference 141..142 disulfide bond formation"
 FT /note= "optionally replaced by Glu-Gly"
 PN WO200105820-A2.
 PD 25-JAN-2001.
 PP 20-JUL-2000; 2000WO-DK00413.
 PR 20-JUL-1999; 99DK-0001014.
 PR 26-JUL-1999; 99US-0145275.
 PA (MEBI-) M & E BIOTECH AS.

XX Halkier T, Mouritsen S, Klysner S;
 XX WPI; 2001-112660/12.
 DR Increasing the muscle mass of animals used in meat production by down
 XX regulating growth differentiation factor 8 (GDF-8) activity in the
 XX animal through induction of anti-GDF-8 antibody production
 XX Example 1; Page 107-108; 110pp; English.
 PS The present sequence is that of AutoVac construct GDF-8 ext,
 CC which consists of the C-terminal 160 amino acids of human growth
 CC differentiation factor 8 (GDF-8, see AAF20131) with residues 16-36
 CC substituted by the promiscuous tetanus toxin T-cell epitope P30 (see
 CC AAB20144) and residues 37-51 substituted by tetanus toxin T-cell
 CC epitope P2 (see AAB20143). It is an object of the invention to
 CC produce a recombinant therapeutic vaccine that is capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. The vaccines (see AAB20145-53) are capable
 CC of breaking auto tolerance against autologous GDF-8. They comprise
 CC the C-terminal portion of human GDF-8 in which a portion of the
 CC native sequence is replaced by a T-cell epitope such as P30, with
 CC minimal disturbance of the authentic 3-dimensional structure of
 CC the protein. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity can increase muscle mass by up to at least 45% in cattle,
 CC pigs and poultry used for meat production, reducing the need for
 CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 CC
 SQ Sequence 160 AA;
 Query Match 100.0%; Score 629; DB 22; Length 160;
 Best Local Similarity 100.0%; Pred. No. 4, 2e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDGDHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 60
 DB 52 DFGDGDHSTESRCRRYPLTVDFEAFGMDWIIAPKRYKANYSGGCEVFLOKYPHTL 111
 QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKEQIIYKGIPIAMVVDRCGCS 109
 DB 112 VHOANPRGSAGPCCPTPKMSPINMLYFNKEQIIYKGIPIAMVVDRCGCS 160
 RESULT 9
 AAB73188
 ID AAB73188 standard; Protein; 226 AA.
 AC AAB73188;
 DT 11-MAY-2001 (first entry)
 DE Chicken GDF-8.
 KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
 KW muscular dystrophy; musculoskeletal disease; tissue repair;
 KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
 KW traumatic injury; congestive obstructive pulmonary disease.
 XX Gallus gallus.
 OS Gallus gallus.
 PN WO200112777-A2.
 PP 22-FEB-2001.
 PR 17-AUG-2000; 2000WO-US22884.
 PR 19-AUG-1999; 99US-0376238.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PA Lee S, McPherson AC;
 PI WPI; 2001-211209/21.
 DR N-PSDB; AAF63554.
 XX New substantially purified growth differentiation factor-8 polypeptide,
 PT useful for treating muscle wasting disease, obesity, muscular
 PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
 PT and cachexia -
 XX
 PS Example 9; Fig 2; 124pp; English.
 XX The present invention relates to growth differentiation factor-8 (GDF-8)
 CC coding sequences and proteins. The present sequence is a GDF-8 protein,
 CC which was isolated in the present invention. GDF-8 is useful for treating
 CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
 CC muscular dystrophy), musculoskeletal diseases or in tissue repair due
 CC to trauma, obesity and disorders related to abnormal proliferation of
 CC adipocytes. GDF-8 is also useful for treating malignancies of the various
 CC organ systems, particularly cells in muscle or adipose tissues and in
 CC gene therapy for the treatment of cell proliferative or immunological
 CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
 CC treating muscle wasting disease, neuromuscular disorder, spinal cord
 CC injury, traumatic injury, congestive obstructive pulmonary disease
 CC (COPD), AIDS or cachexia.
 XX
 SQ Sequence 226 AA;
 Query Match 100.0%; Score 629; DB 22; Length 226;
 Best Local Similarity 100.0%; Pred. No. 6, 2e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTSRRCRPLTVDFEAFGMDWIIARRYKANYGSGCEFFLQKYPHTL 60
 Db 118 DFGDDEHSTSRRCRPLTVDFEAFGMDWIIARRYKANYGSGCEFFLQKYPHTL 177
 QY 61 VHOANFRGSGAPCCPTPMSPINMLYNGKEQIITGKIPAMVVRCCGS 109
 Db 178 VHOANFRGSGAPCCPTPMSPINMLYNGKEQIITGKIPAMVVRCCGS 226
 RESULT 10
 AAB20152
 ID AAB20152 standard; Protein; 254 AA.
 XX AAB20152;
 AC 30-APR-2001 (first entry)
 XX
 DT Growth differentiation factor 8 AutoVac construct GDF-8 dimer.
 XX
 DE Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
 XX T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
 KW cardiant; human; mutant; mutein.
 XX
 OS Chimeric - Homo sapiens.
 OS Chimeric - Clostridium tetrani.
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT /note= "109 C-terminal residues of human GDF-8"
 FT Region
 FT /note= "tetanus toxoid P2 epitope"
 FT Region
 FT /note= "tetanus toxoid P30 epitope"
 FT Region
 FT /note= "109 C-terminal residues of human GDF-8"
 FT /note= 90..91
 FT Misc-difference
 FT /note= "optionally replaced by Glu-Gly"

FT Misc-difference 235..236
 FT /note= "optionally replaced by Glu-Gly"
 XX
 XX W0200105820-A2.
 XX
 XX 25-JAN-2001.
 XX
 XX 20-JUL-2000; 2000WO-DK00413.
 XX
 XX 20-JUL-1999; 99DK-0001014.
 XX 26-JUL-1999; 99US-0145275.
 XX
 XX (MEBI-) M & E BIOTECH AS.
 XX
 XX Halkier T, Mouritsen S, Klysner S;
 XX WPI; 2001-112680/12.
 XX
 DR Increasing the muscle mass of animals used in meat production by down
 FT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 XX
 XX Example 1; Page 105-106; 110pp; English.
 XX
 XX The present sequence is that of AutoVac construct GDF-8 dimer
 CC comprising 2 copies of the 109-amino acid C-terminal region of human
 CC growth differentiation factor 8 (GDF-8; see AAF20141) covalently
 CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)
 CC of tetanus toxin. It is an object of the invention to produce a
 CC recombinant therapeutic vaccine that is capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. The vaccines (see AAB20145-53) are capable
 CC of breaking autoimmunity against autologous GDF-8. They comprise
 CC the C-terminal portion of human GDF-8 in which a portion of the
 CC native sequence is replaced by a T-cell epitope such as P30 with
 CC minimal disturbance of the authentic 3-dimensional structure of
 CC the protein. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity can increase muscle mass by up to at least 45% in cattle,
 CC pigs and poultry used for meat production, reducing the need for
 CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
 CC treat human diseases such as cancer cachexia where muscle atrophy is
 CC pronounced and for patients suffering from acute and chronic heart
 CC failure.
 CC
 XX
 XX Sequence 254 AA;
 SQ
 Query Match 100.0%; Score 629; DB 22; Length 254;
 Best Local Similarity 100.0%; Pred. No. 7e-60;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGDDEHSTSRRCRPLTVDFEAFGMDWIIARRYKANYGSGCEFFLQKYPHTL 60
 Db 146 DFGDDEHSTSRRCRPLTVDFEAFGMDWIIARRYKANYGSGCEFFLQKYPHTL 205
 QY 61 VHOANFRGSGAPCCPTPMSPINMLYNGKEQIITGKIPAMVVRCCGS 109
 Db 206 VHOANFRGSGAPCCPTPMSPINMLYNGKEQIITGKIPAMVVRCCGS 254
 RESULT 11
 AAB20132
 ID AAB20132 standard; Protein; 362 AA.
 XX AAB20132;
 AC 30-APR-2001 (first entry)
 XX
 DT Turkey growth differentiation factor 8.
 XX
 DE Growth differentiation factor 8.
 XX
 KW Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
 KW vaccine; muscle; meat; cachexia; cardiant; turkey.
 XX

OS Melegritis gallopavo.
 XX
 PN MO200105820-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-DK00413.
 XX
 PR 20-JUL-1999; 99DK-0001014.
 PR 26-JUL-1999; 99US-0145275.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 XX
 PI Halkier T, Mouritsen S, Rysner S;
 XX WPI; 2001-112680/12.
 DR
 PT Increasing the muscle mass of animals used in meat production by down
 PT regulating growth differentiation factor 8 (GDF-8) activity in the
 PT animal through induction of anti-GDF-8 antibody production -
 XX
 PS Example 1; Page 76-78; 110pp; English.
 XX
 CC The present sequence is that of turkey growth differentiation factor
 CC 8 (GDF-8), also called myostatin. It is an object of the invention
 CC to produce a recombinant therapeutic vaccine capable of effecting
 CC down-regulation of GDF-8 in order to increase the muscle growth
 CC rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
 CC provided that are capable of breaking autotolerance against
 CC analogous GDF-8. These comprise a C-terminal portion of human
 CC GDF-8 in which a portion of the native sequence is replaced by a
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
 CC P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
 CC for genetic immunisation of the animals. Down-regulation of GDF-8
 CC activity is used to increase muscle mass by up to at least 45%
 CC in cattle, pigs and poultry used for meat production, reducing the
 CC need for antibiotic feed-additives. Anti-GDF8 vaccines can be used
 CC to treat human diseases such as cancer cachexia where muscle atrophy
 CC is pronounced and for patients suffering from acute and chronic
 CC heart failure.
 CC
 SQ Sequence 362 AA;
 XX
 XX
 Query Match 100.0%; Score 629; DB 22; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 254 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 313
 QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGKEQIIYGIKIPAMVVDRCGS 109
 DB 314 VHOANPRGSAGPCCPTPKMSPINMLYFNGKEQIIYGIKIPAMVVDRCGS 362
 RESULT 12
 AAU75623
 ID AAU75623 standard; Protein; 374 AA.
 XX
 AC AAU75623;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Chicken promyostatin.
 XX
 KM Chicken; promyostatin; immunomodulator; antidepressant; anorectic;
 KM neuroprotective; antidiabetic; growth differentiation factor receptor;
 KM myostatin receptor; GDF; muscle tissue; adipose tissue; cachexia;
 KM wasting disorder; anorexia; muscular dystrophy; neuromuscular disease;
 KM metabolic disorder; obesity; type II diabetes.
 XX
 OS Gallus gallus.

XX
 PN MO200210214-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 26-JUL-2001; 2001WO-US23615.
 XX
 PR 27-JUL-2000; 2000US-0626896.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Lee S, McPherron AC;
 XX WPI; 2002-217116/27.
 DR N-PSDB; ABR15396.
 XX
 PT New growth differentiation factor (GDF) receptors and modulators.
 PT useful for ameliorating wasting disorders such as cachexia, muscular
 PT dystrophy or neuromuscular disease or a metabolic disorder such as
 PT obesity or type II diabetes -
 XX
 PS Claim 22; Fig 1; 184pp; English.
 XX
 CC The invention relates to a substantially purified growth differentiation
 CC factor (GDF) receptor, specifically a myostatin receptor, or its
 CC functional peptide portion. Also described is a method of modulating an
 CC effect of myostatin on a cell by contacting the cell with an agent that
 CC affects myostatin signal transduction in the cell. The method and the
 CC receptor are useful for ameliorating the severity of a pathological
 CC condition characterised by an abnormal amount, development or metabolic
 CC activity of muscle or adipose tissue in a subject, particularly a wasting
 CC disorder (e.g. cachexia, anorexia, muscular dystrophy or neuromuscular
 CC disease) or a metabolic disorder (e.g. obesity or type II diabetes). The
 CC present sequence represents the amino acid sequence of chicken
 CC promyostatin.
 CC
 SQ Sequence 374 AA;
 XX
 XX
 Query Match 100.0%; Score 629; DB 23; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.1e-59;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
 DB 266 DFGLDCEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 325
 QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNGKEQIIYGIKIPAMVVDRCGS 109
 DB 326 VHOANPRGSAGPCCPTPKMSPINMLYFNGKEQIIYGIKIPAMVVDRCGS 374
 RESULT 13
 AAR63160
 ID AAR63160 standard; Protein; 375 AA.
 XX
 AC AAR63160;
 XX
 DT 23-JUN-1995 (first entry)
 XX
 DE Human growth differentiation factor-8 protein.
 XX
 KM Growth differentiation factor-8; GDF-8; cell proliferation;
 KM adipocyte; obesity; transforming growth factor-beta.
 XX
 OS Homo sapiens.
 XX
 PN WO9421681-A.
 XX
 PD 29-SEP-1994.
 XX
 PF 18-MAR-1994; 94WO-US03019.
 XX
 PR 19-MAR-1993; 93US-0033923.

```

XX (UYUO ) UNIV JOHNS HOPKINS SCHOOL MED.
PA
XX Lee S, Mcpherron AC;
PI
XX WPI; 1994-316943/39.
DR Q-PSDB; Q76372.
XX
XX New growth differentiation factor 8 - useful for treatment and
PT diagnosis of cell proliferative disorders esp. of muscle.
PS Claim 3; Page 58; 84pp; English.
XX
XX GDF-8 can be used to maintain cells before transplantation; to
CC improve efficiency of cell fusion and to treat obesity or diseases
CC related to abnormal adipocyte proliferation.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 629; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRRYPITVDPEAFGMDWIIAPRRYKANYSGCEFEVFLQKYPHTHL 60
DB 267 DFGLDDEHSTESRCRRYPITVDPEAFGMDWIIAPRRYKANYSGCEFEVFLQKYPHTHL 326

QY 61 VHOANPRGSAGPCCPTPKSPINMLYFNGKEQIITYKIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPKSPINMLYFNGKEQIITYKIKIPAMVVDRCGCS 375

RESULT 14
AAW69888
ID AAW69888 standard; Protein; 375 AA.
XX
AC AAW69888;
XX
DT 07-DEC-1998 (first entry)
XX
DE Chicken growth differentiation factor-8.
XX
KW Growth differentiation factor-8; GDF-8; chicken; transgenic animal;
KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
KW therapy.
XX
OS Gallus sp.
XX
FH Key Location/Qualifiers
FT Cleavage-site 263..266
FT Protein 267..375
FT /label= Mat_protein
XX
PN WO9833887-A1.
XX
PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US02479.
XX
PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.
PR 28-APR-1997; 97US-0847910.
XX
PA (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, Mcpherron AC;
XX
DR WPI; 1998-437444/37.
DR N-PSDB; AAV45819.
XX
XX Transgenic animals with gene for growth differentiation factor-8
PT disrupted - have increased muscle and reduced cholesterol contents,

```

```

PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease
XX
XX Example 9; Fig 14c; 125pp; English.
PS
XX
XX This is the amino acid sequence of chicken growth differentiation
CC factor-8 (GDF-8), a novel member of the transforming growth factor-
CC beta superfamily that appears to relate to various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. The sequence was deduced from a cDNA clone
CC (see AAV45819) isolated from a skeletal muscle cDNA library. The
CC invention provides novel mammalian and avian GDF-8 proteins (see
CC AAW69883-92). A transgenic non-human animal is claimed in which
CC GDF-8 expression is disrupted or interfered with. Also claimed
CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
CC from these animals; (2) method for increasing muscle mass in
CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
CC inhibiting the action of GDF-8 by treating foetal or adult muscle
CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
CC active fragment. The transgenic animals have increased muscle mass
CC and for poultry reduced cholesterol contents. Method (3) is used
CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
CC and aging, particularly muscular dystrophy, spinal cord or
CC traumatic injuries, congestive or obstructive lung disease, AIDS
CC and cachexia. Method (4) is used to treat cancer of muscle,
CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
CC can be used to maintain myoblasts intended for transplanting or to
CC improve efficiency of fusion. Ab can be used to detect and
CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
CC also for immunotherapy and in vivo imaging.
XX
SQ Sequence 375 AA;

Query Match 100.0%; Score 629; DB 19; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGLDDEHSTESRCRRYPITVDPEAFGMDWIIAPRRYKANYSGCEFEVFLQKYPHTHL 60
DB 267 DFGLDDEHSTESRCRRYPITVDPEAFGMDWIIAPRRYKANYSGCEFEVFLQKYPHTHL 326

QY 61 VHOANPRGSAGPCCPTPKSPINMLYFNGKEQIITYKIKIPAMVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPKSPINMLYFNGKEQIITYKIKIPAMVVDRCGCS 375

RESULT 15
AAW69891
ID AAW69891 standard; Protein; 375 AA.
XX
AC AAW69891;
XX
DT 07-DEC-1998 (first entry)
XX
DE Pig growth differentiation factor-8.
XX
KW Growth differentiation factor-8; GDF-8; pig; transgenic animal;
KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
KW therapy.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT Cleavage-site 263..266
FT Protein 267..375
FT /label= Mat_protein
XX
PN WO9833887-A1.
XX
PD 06-AUG-1998.
XX

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PF 05-FEB-1998; 98WO-US02479.
 XX
 PR 23-MAY-1997; 97US-0862445.
 PR 05-FEB-1997; 97US-0795071.
 PR 28-APR-1997; 97US-0847910.
 XX
 PA (UY00) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Lee S, McPherron AC;
 XX
 DR MPI; 1998-437444/37.
 DR N-PSDB; AAV45822.
 XX
 PT Transgenic animals with gene for growth differentiation factor-8
 PT disrupted - have increased muscle and reduced cholesterol contents,
 PT also use of GDF-8 inhibitors for treating cancer, obesity,
 PT neuromuscular disease
 XX
 PS Example 9; Fig 14f; 125bp; English.
 CC
 CC This is the amino acid sequence of porcine growth differentiation
 CC factor-8 (GDF-8), a novel member of the transforming growth factor-
 CC beta superfamily that appears to relate to various cell
 CC proliferative disorders, especially those involving muscle, nerve
 CC and adipose tissue. The sequence was deduced from a cDNA clone
 CC (see AAV45822) isolated from a skeletal muscle cDNA library. The
 CC invention provides novel mammalian and avian GDF-8 proteins (see
 CC AAM69883-92). A transgenic non-human animal is claimed in which
 CC GDF-8 expression is disrupted or interfered with. Also claimed
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb
 CC from these animals; (2) method for increasing muscle mass in
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal
 CC active fragment. The transgenic animals have increased muscle mass
 CC and for poultry reduced cholesterol contents. Method (3) is used
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy
 CC and aging, particularly muscular dystrophy, spinal cord or
 CC traumatic injuries, congestive or obstructive lung disease, AIDS
 CC and cachexia. Method (4) is used to treat cancer of muscle,
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8
 CC can be used to maintain myoblasts intended for transplanting or to
 CC improve efficiency of fusion. Ab can be used to detect and
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),
 CC also for immunotherapy and in vivo imaging.
 CC
 SO Sequence 375 AA:

Query Match 100.0%; Score 629; DB 19; Length 375;

Best Local Similarity 100.0%; Fred. No. 1.1e-59;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDDEHSTSRCCRYPLTVDFEAFQMDWIIAPKRYKANYCSEGCERFLOKYPTHTL 60
 Db 267 DFGIDCDDEHSTSRCCRYPLTVDFEAFQMDWIIAPKRYKANYCSEGCERFLOKYPTHTL 326
 QY 61 VHOANPRGASGPGCTPTTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGS 109
 Db 327 VHOANPRGASGPGCTPTTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGS 375

Search completed: January 31, 2003, 18:20:10
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:20:18 ; Search time 8 Seconds
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274.933 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629

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Scoring table: BLOSUM62

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Searched: 122226 segs, 20178551 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	629	100.0	130	9	US-09-859-211-33
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4	629	100.0	374	9	US-09-841-730-8
5	629	100.0	375	9	US-09-841-730-2
6	629	100.0	375	9	US-09-841-730-14
7	629	100.0	375	9	US-09-841-730-18
8	629	100.0	375	9	US-09-859-211-14
9	629	100.0	375	9	US-09-859-211-23
10	629	100.0	375	9	US-09-859-211-27
11	629	100.0	375	9	US-09-859-211-29
12	629	100.0	375	10	US-09-454-540-5
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14	629	100.0	376	9	US-09-841-730-6
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18	629	100.0	376	10	US-09-859-894A-11
19	624	99.2	375	10	US-09-859-894A-5

20	623	99.0	375	9	US-09-841-730-10	Sequence 10, Appl
21	623	99.0	375	9	US-09-859-211-19	Sequence 19, Appl
22	622	98.9	109	10	US-09-754-826-2	Sequence 2, Appl
23	619	98.4	375	9	US-09-841-730-16	Sequence 16, Appl
24	619	98.4	375	9	US-09-859-211-31	Sequence 31, Appl
25	618	98.3	375	9	US-09-841-730-12	Sequence 12, Appl
26	618	98.3	375	9	US-09-859-211-21	Sequence 21, Appl
27	590	93.8	108	9	US-09-859-211-8	Sequence 8, Appl
28	581	92.4	126	10	US-09-454-540-4	Sequence 4, Appl
29	581	92.4	126	10	US-09-859-894A-4	Sequence 4, Appl
30	581	92.4	407	9	US-09-841-730-25	Sequence 25, Appl
31	581	92.4	407	10	US-09-454-540-2	Sequence 2, Appl
32	581	92.4	407	10	US-09-454-540-6	Sequence 6, Appl
33	581	92.4	407	10	US-09-859-894A-2	Sequence 2, Appl
34	581	92.4	408	9	US-09-813-398-33	Sequence 3, Appl
35	570	90.6	374	9	US-09-841-730-20	Sequence 20, Appl
36	564	89.7	136	9	US-09-841-730-29	Sequence 29, Appl
37	564	89.7	157	9	US-09-841-730-27	Sequence 27, Appl
38	512.5	81.5	128	10	US-09-205-658-317	Sequence 317, App
39	242	38.5	120	10	US-09-813-459-20	Sequence 20, Appl
40	242	38.5	120	12	US-10-115-406-20	Sequence 40, Appl
41	242	38.5	121	9	US-09-859-211-46	Sequence 46, Appl
42	242	38.5	121	9	US-09-880-708-24	Sequence 24, Appl
43	242	38.5	408	9	US-09-813-398-20	Sequence 20, Appl
44	242	38.5	408	9	US-09-813-398-22	Sequence 22, Appl
45	232.5	37.0	118	12	US-10-115-406-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-859-211-6
; Sequence 6, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; CURRENT FILING DATE: 2001-05-15
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-859-211-6

Query Match 100.0%; Score 629; DB 9; Length 126;

Best local Similarity 100.0%; Pred. No. 1.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-859-211-33
; Sequence 33, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-859-211-33

Query Match      100.0%; Score 629; DB 9; Length 130;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db      22  DFGDGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEVFLOKYPHTL 81
|||||

Qy      61  VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
|||||
Db      82  VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 130
|||||

RESULT 3
US-09-859-211-35
; Sequence 35, Application US/09859211
; Patent No. US20020157125A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; FILE REFERENCE: 07265/144001
; CURRENT APPLICATION NUMBER: US/09/859,211
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/019,070
; PRIOR FILING DATE: 1998-02-05
; PRIOR APPLICATION NUMBER: 08/862,445
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 08/847,910
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/795,071
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 08/525,596
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: PCT/US94/03019
; PRIOR FILING DATE: 1994-03-18
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; PRIOR APPLICATION NUMBER: 08/033,923
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-859-211-35

Query Match      100.0%; Score 629; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.5e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DFGDGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEVFLOKYPHTL 60
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Db      118 DFGDGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEVFLOKYPHTL 177
|||||

Qy      61  VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
|||||
Db      178 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 226
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RESULT 4
US-09-841-730-8
; Sequence 8, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; FILE REFERENCE: JHU470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-841-730-8

Query Match      100.0%; Score 629; DB 9; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DFGDGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEVFLOKYPHTL 60
|||||
Db      266 DFGDGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPRYKANYCSGCEVFLOKYPHTL 325
|||||

Qy      61  VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 109
|||||
Db      326 VHOANPRGSAGPCTPTKMSPINMLYFNKGEOIITYGKIPAMVVDRCGCS 374
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RESULT 5
US-09-841-730-2
; Sequence 2, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
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FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-841-730-2

Query Match          100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5,9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 60
267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
DB 267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 375

RESULT 6
US-09-841-730-14
Sequence 14, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 375
TYPE: PRT
ORGANISM: Porcine
US-09-841-730-14

Query Match          100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5,9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 60
267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
DB 267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 375
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RESULT 7
US-09-841-730-18
Sequence 18, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
FILE REFERENCE: JH01470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 375
TYPE: PRT
ORGANISM: Meleagris gallopavo
US-09-841-730-18

Query Match          100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5,9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 60
267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
DB 267 DFGLDDEHSTESRCRRYPLTVDFEAFGWDWIIAPKRYKANYCSGCEVFLOKYPHTL 326
QY 61 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCPTPTMSPINMLYFNKGEOIYIGKIPANVVDRCGCS 375

RESULT 8
US-09-859-211-14
Sequence 14, Application US/09859211
Patent No. US20020157125A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
FILE REFERENCE: 07265/14401
CURRENT APPLICATION NUMBER: US/09/859,211
CURRENT FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/019,070
PRIOR FILING DATE: 1998-02-05
PRIOR APPLICATION NUMBER: 08/862,445
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 08/847,910
PRIOR FILING DATE: 1997-04-28
PRIOR APPLICATION NUMBER: 08/795,071
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: 08/525,596
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: PCT/US94/03019
PRIOR FILING DATE: 1994-03-18
PRIOR APPLICATION NUMBER: 08/033,923
PRIOR FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-859-211-14
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Sun Feb 2 11:34:27 2003

us-09-620-586b-11.rapb

Page 4

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Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 60
Db 267 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 326

Qy 61 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 109
Db 327 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 375

RESULT 9
US-09-859-211-23
/ Sequence 23, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: McPherson, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 23
/ LENGTH: 375
/ TYPE: PRT
/ ORGANISM: Gallus gallus
/ US-09-859-211-23

Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 60
Db 267 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 326

Qy 61 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 109
Db 327 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 375

RESULT 10
US-09-859-211-27
/ Sequence 27, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: McPherson, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
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/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 375
/ TYPE: PRT
/ ORGANISM: Meleagris gallopavo
/ US-09-859-211-27

Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 60
Db 267 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 326

Qy 61 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 109
Db 327 VHOANRPSGAGPCCTPTKMSPINMLYFNKGEOIYIKIPAMVVDRCGCS 375

RESULT 11
US-09-859-211-29
/ Sequence 29, Application US/09859211
/ Patent No. US20020157125A1
/ GENERAL INFORMATION:
/ APPLICANT: McPherson, Alexandra C.
/ TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
/ FILE REFERENCE: 07265/144001
/ CURRENT FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 09/019,070
/ PRIOR FILING DATE: 1998-02-05
/ PRIOR APPLICATION NUMBER: 08/862,445
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 08/847,910
/ PRIOR FILING DATE: 1997-04-28
/ PRIOR APPLICATION NUMBER: 08/795,071
/ PRIOR FILING DATE: 1997-02-05
/ PRIOR APPLICATION NUMBER: 08/525,596
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: PCT/US94/03019
/ PRIOR FILING DATE: 1994-03-18
/ PRIOR APPLICATION NUMBER: 08/033,923
/ PRIOR FILING DATE: 1993-03-19
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 29
/ LENGTH: 375
/ TYPE: PRT
/ ORGANISM: Porcine
/ US-09-859-211-29

Query Match 100.0%; Score 629; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 60
Db 267 DFGIDCDHSTSRCCRYPLTVDFEAFGMDWIIAPKRYKANYCGCECFVLOKYPHTL 326
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QY 61 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 327 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 375

RESULT 12
US-09-454-540-5
Sequence 5, Application US/09454540
Patent No. US20010053358A1
GENERAL INFORMATION:
APPLICANT: Se-jin Lee and Alexandra McPherron
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/454,540
FILING DATE: 06-DEC-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HATLE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GFP-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-09-454-540-5
Query Match 100.0%; Score 629; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 60
DB 267 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 326

QY 61 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 327 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 375

RESULT 13
US-09-841-730-4
Sequence 4, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:

APPLICANT: Lee, Se-jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 376
TYPE: PRT
ORGANISM: Mus musculus
US-09-841-730-4
Query Match 100.0%; Score 629; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 60
DB 268 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 327

QY 61 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 328 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 376

RESULT 14
US-09-841-730-6
Sequence 6, Application US/09841730
Patent No. US20020157126A1
GENERAL INFORMATION:
APPLICANT: Lee, Se-jin
APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
FILE REFERENCE: JHU470-2
CURRENT APPLICATION NUMBER: US/09/841,730
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/626,896
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 09/485,046
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: PCT/US98/15598
PRIOR FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: 60/054,461
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 376
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-841-730-6
Query Match 100.0%; Score 629; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 5.9e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 60
DB 268 DFGIDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCEGFVLOKYPHTHL 327

QY 61 VHQAHPGASAGPCTPTKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109

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OM protein - protein search, using sw model

Run on: January 31, 2003, 18:17:50 ; Search time 11.5 Seconds
(without alignments)
278.878 Million cell updates/sec

Title: US-09-620-586B-11

Perfect score: 629

Sequence: 1 DFGDCDHESTESRCRCRYPL.....KEQIYKIPAMVYDRGCS 109

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	629	100.0	126	2	US-08-525-596B-6
2	629	100.0	126	3	US-09-177-860A-6
3	629	100.0	126	4	US-09-378-238-6
4	629	100.0	126	4	US-09-451-501-6
5	629	100.0	130	4	US-09-378-238-21
6	629	100.0	225	4	US-09-378-238-19
7	629	100.0	375	2	US-08-525-596B-14
8	629	100.0	375	2	US-08-765-875-5
9	629	100.0	375	3	US-08-795-671-5
10	629	100.0	375	3	US-09-177-860A-14
11	629	100.0	375	4	US-09-252-149B-29
12	629	100.0	375	4	US-09-252-149B-32
13	629	100.0	375	4	US-09-252-149B-34
14	629	100.0	375	4	US-09-252-149B-35
15	629	100.0	375	4	US-09-378-238-14
16	629	100.0	375	4	US-09-451-501-14
17	629	100.0	375	4	US-09-451-501-19
18	629	100.0	375	4	US-09-451-501-21
19	629	100.0	375	4	US-09-451-501-23
20	629	100.0	375	4	US-09-451-501-27
21	629	100.0	376	2	US-08-525-596B-12
22	629	100.0	376	3	US-09-177-860A-11
23	629	100.0	376	3	US-08-891-789B-6
24	629	100.0	376	4	US-09-252-149B-27
25	629	100.0	376	4	US-09-252-149B-28
26	629	100.0	376	4	US-09-378-238-12
27	629	100.0	376	4	US-09-451-501-12

28	629	100.0	376	4	US-09-451-501-25	Sequence 25, Appl
29	623	99.0	375	4	US-09-252-149B-30	Sequence 30, Appl
30	619	98.4	375	4	US-09-252-149B-33	Sequence 33, Appl
31	618	98.3	375	3	US-08-891-789B-2	Sequence 2, Appl
32	618	98.3	375	4	US-09-252-149B-2	Sequence 2, Appl
33	618	98.3	375	4	US-09-252-149B-31	Sequence 31, Appl
34	590	93.8	108	2	US-09-525-596B-8	Sequence 8, Appl
35	590	93.8	108	3	US-09-177-860A-8	Sequence 8, Appl
36	590	93.8	108	4	US-09-378-238-8	Sequence 8, Appl
37	590	93.8	108	4	US-09-451-501-8	Sequence 8, Appl
38	581	92.4	126	1	US-08-247-907A-2	Sequence 2, Appl
39	581	92.4	126	1	US-08-452-772-2	Sequence 2, Appl
40	581	92.4	126	2	US-08-765-875-4	Sequence 4, Appl
41	581	92.4	126	3	US-08-765-871-4	Sequence 4, Appl
42	581	92.4	126	4	US-09-414-234-2	Sequence 2, Appl
43	581	92.4	126	4	US-08-919-850-2	Sequence 2, Appl
44	581	92.4	126	5	PCT-US94-05288-2	Sequence 2, Appl
45	581	92.4	362	1	US-08-247-907A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-525-596B-6
; Sequence 6, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-ujin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-525-596B-6
Query Match 100.0%; Score 629; DB 2; Length 126;
Best local similarity 100.0%; Pred. No. 3,7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 DFGDCDHESTESRCRCRYPLTVDFEAFGMDWIAPRYKANCSCGCEPFLQKYPHTL 60
|||||

Db 18 DFGDCEHSTESRCRYPITVDPEAFGMDWIAPRYKANYCSECEFFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 109

Db 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 126

RESULT 2

US-09-177-860A-6
Sequence 6, Application US/09177860A
Patent No. 6096506

GENERAL INFORMATION:
APPLICANT: Huynh Thanh

APPLICANT: Lee, Se-jin

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995

ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003

TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

US-09-177-860A-6

Query Match 100.0%; Score 629; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 3,7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPITVDPEAFGMDWIAPRYKANYCSECEFFVLOKYPHTL 60

Db 18 DFGDCEHSTESRCRYPITVDPEAFGMDWIAPRYKANYCSECEFFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 109

Db 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 126

RESULT 3

US-09-378-238-6
Sequence 6, Application US/09378238
Patent No. 6465239

GENERAL INFORMATION:
APPLICANT: Lee, Se-jin

APPLICANT: McPherron, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN

TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES

FILE REFERENCE: JHU1120-9

CURRENT APPLICATION NUMBER: US/09/378,238

CURRENT FILING DATE: 1999-08-19

EARLIER APPLICATION NUMBER: 08/795,071

EARLIER FILING DATE: 1997-02-05

EARLIER APPLICATION NUMBER: 08/525,596

EARLIER FILING DATE: 1995-10-25

EARLIER APPLICATION NUMBER: PCT/US94/03019

EARLIER FILING DATE: 1994-03-18

EARLIER APPLICATION NUMBER: 08/033,923

EARLIER FILING DATE: 1993-03-19

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 126

TYPE: PRT

ORGANISM: Mus musculus

US-09-378-238-6

Query Match 100.0%; Score 629; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 3,7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDCEHSTESRCRYPITVDPEAFGMDWIAPRYKANYCSECEFFVLOKYPHTL 60

Db 18 DFGDCEHSTESRCRYPITVDPEAFGMDWIAPRYKANYCSECEFFVLOKYPHTL 77

QY 61 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 109

Db 78 VHOANPRGSAGPCCPTPTKMSPINMLYFNKKEQIITYGKIPAMVVDRCGCS 126

RESULT 4

US-09-451-501-6
Sequence 6, Application US/09451501
Patent No. 6468535

GENERAL INFORMATION:
APPLICANT: Se-jin Lee et al.,
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,501
FILING DATE: 30-NOV-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,071
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US94/03019
FILING DATE: 18-March-1994

ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/105001

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-451-501-6

Query Match 100.0%; Score 629; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 3.7e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 18 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 77
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 78 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 126

RESULT 5

US-09-378-238-21
Sequence 21, Application US/09378238
Patent No. 6465239

GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JH01120-9

CURRENT APPLICATION NUMBER: US/09/378,238
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21

LENGTH: 130
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-378-238-21

Query Match 100.0%; Score 629; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 3.8e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 22 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 81

QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 82 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 130

RESULT 6

US-09-378-238-19
Sequence 19, Application US/09378238
Patent No. 6465239

GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: McPherson, Alexandra C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
FILE REFERENCE: JH01120-9
CURRENT APPLICATION NUMBER: US/09/378,238

CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 08/795,071
EARLIER FILING DATE: 1997-02-05
EARLIER APPLICATION NUMBER: 08/525,596
EARLIER FILING DATE: 1995-10-25
EARLIER APPLICATION NUMBER: PCT/US94/03019
EARLIER FILING DATE: 1994-03-18
EARLIER APPLICATION NUMBER: 08/033,923
EARLIER FILING DATE: 1993-03-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 225
TYPE: PRT
ORGANISM: Gallus gallus
US-09-378-238-19

Query Match 100.0%; Score 629; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.3e-66;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 60
DB 117 DFGDLCDEHSTESRCRYPLTVDFEAFGMDWIIAPKRYKANYCSGCECFVFLQKYPHTL 176
QY 61 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 109
DB 177 VHOANPRGSAGPCCPTPKMSPINMLYFNKGEOIYIGKIPAMVVDRCGCS 225

RESULT 7

US-08-525-596B-14
Sequence 14, Application US/08525596B
Patent No. 5827733

GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US

ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,596B
FILING DATE: 19-SEP-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D, John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: 07265/075001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5099
TELEFAX: 619-678-5070

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-525-596B-14

Query Match 100.0%; Score 629; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 60
DB 267 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 375

RESULT 8

US-08-765-875-5
Sequence 5, Application US/08765875
Patent No. 5914234
GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: MCPHERON, ALEXANDRA C.
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,875
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/706,958
FILING DATE:
APPLICATION NUMBER: US/08/272,763
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN PH.D., LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3641
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GFP-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-765-875-5

Query Match 100.0%; Score 629; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 60
DB 267 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 326

QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 375

RESULT 9

US-08-795-671-5
Sequence 5, Application US/08795671
Patent No. 6008434
GENERAL INFORMATION:
APPLICANT: Se-jin Lee and Alexandra McPherson
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,671
FILING DATE: February 6, 1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/106001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: GFP-8
FEATURE:
NAME/KEY: Protein
LOCATION: 1..375
US-08-795-671-5

Query Match 100.0%; Score 629; DB 3; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 60
DB 267 DFGDGDCHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYGSGCEGFVFLQKYPHTHL 326
QY 61 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 109
DB 327 VHQANPRGSAGPCCTPTKMSPINMLYFNKGEOIIVGKIPAMVVDRCGCS 375

RESULT 10

US-09-177-860A-14
Sequence 14, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

Sun Feb 2 11:34:26 2003

us-09-620-586b-11.ra1

Page 5

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ADDRESS: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07665/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-177-860A-14

Query Match
Best Local Similarity 100.0%; Score 629; DB 3; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 60
DB 267 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 375

RESULT 11
US-09-252-149B-29
Sequence 29, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-252-149B-29

Query Match
Best Local Similarity 100.0%; Score 629; DB 4; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 60
DB 267 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 375

RESULT 12
US-09-252-149B-32
Sequence 32, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 375
TYPE: PRT
ORGANISM: Sus scrofa
US-09-252-149B-32

Query Match
Best Local Similarity 100.0%; Score 629; DB 4; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 60
DB 267 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 326
QY 61 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 109
DB 327 VHOANPRGSAGPCCTPTTMSPIINMLYFNGKEQIIYGIKIPANVVDRCGCS 375

RESULT 13
US-09-252-149B-34
Sequence 34, Application US/09252149B
Patent No. 6369201
GENERAL INFORMATION:
APPLICANT: Barker, Christopher A.
TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULAR MYOSTATIN IN
FILE REFERENCE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/075,213
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 375
TYPE: PRT
ORGANISM: Gallus gallus
US-09-252-149B-34

Query Match
Best Local Similarity 100.0%; Score 629; DB 4; Length 375;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 60
DB 267 DFGDDCDHEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANYCGSGCEPFVLOKYPHTL 326
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Sun Feb 2 11:34:26 2003

us-09-620-586b-11.ra1

Page 6

Oy 61 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 109
Db 327 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 375

RESULT 14
US-09-252-149B-35
; Sequence 35, Application US/09252149B
; Patent No. 6369201
; GENERAL INFORMATION:
; APPLICANT: Barker, Christopher A.
; APPLICANT: Morsey, Mohamed
; TITLE OF INVENTION: IMMUNOLOGICAL METHODS TO MODULATE MYOSTATIN IN
; TITLE OF INVENTION: VERTEBRATE SUBJECTS
; FILE REFERENCE: 9001-0042
; CURRENT APPLICATION NUMBER: US/09/252,149B
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/075,213
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Melaleuca gallopavo
US-09-252-149B-35

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1,3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 267 DFGDCCDEHSTESRCRYPPLTYDPEAFGMDWIIAPKRYKANYSGCECFVFIQKYPHTL 326
Oy 61 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 109
Db 327 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 375

RESULT 15
US-09-378-238-14
; Sequence 14, Application US/09378238
; Patent No. 6465239
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-jin
; APPLICANT: McPherson, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8 NUCLEIC
; TITLE OF INVENTION: ACID AND POLYPEPTIDES FROM AQUATIC SPECIES AND NON-HUMAN
; TITLE OF INVENTION: TRANSGENIC AQUATIC SPECIES
; FILE REFERENCE: JH01120-9
; CURRENT APPLICATION NUMBER: US/09/378,238
; PRIOR FILING DATE: 1999-08-19
; EARLIER APPLICATION NUMBER: 08/795,071
; EARLIER FILING DATE: 1997-02-05
; EARLIER APPLICATION NUMBER: 08/525,596
; EARLIER FILING DATE: 1995-10-25
; EARLIER APPLICATION NUMBER: PCT/US94/03019
; EARLIER FILING DATE: 1994-03-18
; EARLIER APPLICATION NUMBER: 08/033,923
; EARLIER FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-378-238-14

Query Match 100.0%; Score 629; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1,3e-65;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 267 DFGDCCDEHSTESRCRYPPLTYDPEAFGMDWIIAPKRYKANYSGCECFVFIQKYPHTL 326
Oy 61 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 109
Db 327 VHOANPRGSAAGCCTPTKMSPIIMLYENGEKQIITYGKIPAMVYDRGCS 375

Search completed: January 31, 2003, 18:18:23
Job time : 12.5 secs